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From: Saidha, Tekchand
Sent: Tuesday, March 04, 2003 4:00 PM
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Subject: 10/017145 - sequence search request

10/017145 - sequence search request

Please search the data bases and Interference files for :

SEQ ID NO : 1

Thank you,

Tekchand Saidha
Primary Examiner
Art Unit 1652, CM1, Room No. 10D05
Mail Box 10D01
(703) 305-6595

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P. Sheppard
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Searcher: _____
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Other: _____

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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:06:42 ; Search time 33 seconds
(without alignments)
2266.518 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSGSEVENLKKPFMP.....RAKEAPMPFSWIFDRQVKL 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1771	92.4	396	10 Q43140	Q43140 sesamum ind
2	1757	91.7	396	10 Q43141	Q43141 sesamum ind
3	1746	91.1	396	10 Q93X20	Q93X20 sesamum ind
4	1733	90.4	401	10 Q22832	Q22832 arabidopsis
5	1729	90.2	401	10 Q94AE9	Q94AE9 arabidopsis
6	1727	90.1	396	10 Q24497	Q24497 helianthus
7	1701	88.8	396	10 Q24498	Q24498 helianthus
8	1698	88.6	396	10 Q9SEK6	Q9SEK6 persea amer
9	1698	88.6	401	10 Q39355	Q39355 brassica na
10	1696.5	88.5	409	10 Q9SW87	Q9SW87 arachis hyp
11	1695	88.5	401	8 Q9XQR7	Q9XQR7 brassica ju
12	1688	88.1	396	10 Q65040	Q65040 macfadyena
13	1673	87.3	396	10 Q8VXJ7	Q8VXJ7 helianthus
14	1670	87.2	396	10 Q8VXJ8	Q8VXJ8 helianthus
15	1660.5	86.7	407	10 Q42591	Q42591 arabidopsis
16	1653.5	86.3	396	10 Q8S059	Q8S059 oryza sativ

17	1652	86.2	358	10 Q43196	Q43196 thunbergia
18	1637	85.4	396	10 Q9M4N5	Q9M4N5 gossypium h
19	1629	85.0	396	10 Q82014	Q82014 linum usita
20	1620	84.6	396	10 Q9SBA2	Q9SBA2 linum usita
21	1608	83.9	399	10 Q947F1	Q947F1 kochia scop
22	1601	83.6	390	10 Q43197	Q43197 thunbergia
23	1600.5	83.5	396	10 Q9M879	Q9M879 arabidopsis
24	1599	83.5	390	10 Q43198	Q43198 thunbergia
25	1526.5	79.7	394	10 Q9LF04	Q9LF04 arabidopsis
26	1405.5	73.4	386	10 Q947F2	Q947F2 kochia scop
27	1380	72.0	411	10 Q9M881	Q9M881 arabidopsis
28	1358	70.9	401	10 Q9LF05	Q9LF05 arabidopsis
29	1351	70.5	396	10 Q9M880	Q9M880 arabidopsis
30	1318	68.8	374	10 Q9MAR6	Q9MAR6 arabidopsis
31	1315	68.6	384	10 Q9XFC1	Q9XFC1 lupinus lut
32	1261	65.8	387	10 Q41510	Q41510 thunbergia
33	1219.5	63.6	385	10 P92933	P92933 asclepias s
34	1218	63.6	368	10 Q40879	Q40879 pelargonium
35	1009.5	52.7	222	10 Q64906	Q64906 pelargonium
36	771	40.2	167	10 Q43142	Q43142 sesamum ind
37	745	38.9	161	10 Q9XEH1	Q9XEH1 elaeis guin
38	307	16.0	328	16 Q9XAL3	Q9XAL3 streptomyce
39	272	14.2	338	16 Q8VKD4	Q8VKD4 mycobacteri
40	272	14.2	338	16 Q50824	Q50824 mycobacteri
41	267	13.9	338	16 Q50050	Q50050 mycobacteri
42	158	8.2	275	16 Q9X793	Q9X793 mycobacteri
43	142	7.4	170	2 Q9K539	Q9K539 mycobacteri
44	138	7.2	275	16 Q53442	Q53442 mycobacteri
45	126.5	6.6	1349	5 Q9VPR5	Q9VPR5 drosophila

ALIGNMENTS

RESULT 1

ID	Q43140	PRELIMINARY;	PRT;	396 AA.
AC	Q43140;			
DT	01-NOV-1996 (TReMBLrel. 01, Created)			
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)			
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)			
DE	Acyl-[acyl-carrier protein] desaturase precursor (EC 1.14.99.6)			
DE	(Stearoyl-ACP desaturase).			
OS	Sesamum indicum (Oriental sesame) (Gingelly).			
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Assteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.			
OX	NCBI_TaxID=4182;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=4294;			
RX	MEDLINE=96213006; PubMed=8665096;			
RA	Yukawa Y., Takaiwa F., Shoji K., Masuda K., Yamada K.;			
RT	"Structure and expression of two seed-specific cDNA clones encoding			
RT	stearoyl-acyl carrier protein desaturase from sesame, Sesamum indicum			
RT	L.";			
RL	Plant Cell Physiol. 37:201-205(1996)			
CC	-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A			
CC	CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL			
CC	CHAIN (BY SIMILARITY).			
CC	-!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)			
CC	= OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.			
CC	-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY			
CC	SIMILARITY).			
CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY			
CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE			
CC	OILS.			
CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).			
CC	EMBL: D42086; BAA07681.1; -			
DR	HSSP: P22337; IAFR.			
DR	InterPro: IPR005067; FA_desat.			

DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase-2; 1.
 DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
 FT TRANSIT 1 33 POTENTIAL.
 FT CHAIN 34 396 STEAROYL-ACYL CARRIER PROTEIN DESATURASE.
 SQ SEQUENCE 396 AA; 45168 MW; A23475AB676A0940 CRC64;
 Query Match 92.4%; Score 1771; DB 10; Length 396;
 Best Local Similarity 91.2%; Pred. No. 7.6e-137;
 Matches 331; Conservative 20; Mismatches 12; Indels 0; Gaps 0;

QY 1 ASTLKSSEVENLKKPFMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVK 60
 DB 34 ASTLRSGSEVETVKRPFNPREVHVQVTHSMPPQKIEIFKALEWADNNILVHLKPVK 93
 QY 61 CWQPDPLDPASDGDQVRELRLERAKKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120
 DB 94 CWQPDPLDPSSDGDQVKELRERAKKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153
 QY 121 VRDETGAAPTSMWITRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTYOYLIGSGMDPR 180
 DB 154 VRDETGAAPTSMWITRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTYOYLIGSGMDPR 213
 QY 181 TENSPLYGFTYTSFQERATFISHGNTARAKHEGDIKLAQICGTIAADEKRKHETAYTKIV 240
 DB 214 TENSPLYGFTYTSFQERATFISHGNTARAKHEGDIKLAQICGTIAADEKRKHETAYTKIV 273
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRGLGVYAKDYADI 300
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRGLGVYAKDYADI 333
 QY 301 LEFLVGRWKVDKLTGLSAGQKADYVCRLLPPIRLLEERAQRAKEAPMPFSWIFDRQ 360
 DB 334 LEHLVARKVKNLTGLSADGRKAQDYVCGLPPIRLLEERAQRAKAPKIPFSWIHRE 393
 QY 361 VKL 363
 DB 394 VQL 396

RESULT 2
 Q43141 ID Q43141 PRELIMINARY; PRT; 396 AA.
 AC Q43141
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 DE Sesamum indicum (Oriental sesame) (Gingelly).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4294;
 RA Yukawa Y., Takaiwa F., Yamada K.;
 RT "Structure and expression of two cDNA clones encoding stearoyl-acyl carrier protein desaturase in sesame."
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 DR EMBL: D49832; BA08635.1; -;
 DR HSP; P22337; IAPR.
 DR InterPro: IPR005067; FA_desat.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase-2; 1.
 DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
 KW Transit peptide.
 SQ SEQUENCE 396 AA; 45212 MW; 1335DEC4A1B2BF9A CRC64;
 Query Match 91.7%; Score 1757; DB 10; Length 396;
 Best Local Similarity 90.6%; Pred. No. 1.1e-135;
 Matches 329; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 ASTLKSSEVENLKKPFMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVK 60
 DB 34 ASTLRSGSEVETVKRPFNPREVHVQVTHSMPPQKIEIFKALEWADNNILVHLKPVK 93
 QY 61 CWQPDPLDPASDGDQVRELRLERAKKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120
 DB 94 CWQPDPLDPSSDGDQVKELRERAKKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153
 QY 121 VRDETGAAPTSMWITRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTYOYLIGSGMDPR 180
 DB 154 VRDETGAAPTSMWITRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTYOYLIGSGMDPR 213
 QY 181 TENSPLYGFTYTSFQERATFISHGNTARAKHEGDIKLAQICGTIAADEKRKHETAYTKIV 240
 DB 214 TENSPLYGFTYTSFQERATFISHGNTARAKHEGDIKLAQICGTIAADEKRKHETAYTKIV 273
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRGLGVYAKDYADI 300
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRGLGVYAKDYADI 333
 QY 301 LEFLVGRWKVDKLTGLSAGQKADYVCRLLPPIRLLEERAQRAKEAPMPFSWIFDRQ 360
 DB 334 LEHLVARKVKNLTGLSADGRKAQDYVCGLPPIRLLEERAQRAKAPKIPFSWIHRE 393
 QY 361 VKL 363
 DB 394 VQL 396

RESULT 3
 Q93X20 ID Q93X20 PRELIMINARY; PRT; 396 AA.
 AC Q93X20
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Stearyl acyl carrier protein.
 OS Sesamum indicum (Oriental sesame) (Gingelly).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=DEVELOPING SEED;
 RA Kanrar S.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=DEVELOPING SEED;
 RA Chopra V.L.;
 RT "Transgenic expression of cDNA encoding stearyl acyl carrier protein desaturase of sesamum indicum in Indian mustard."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

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RC TISSUE=DEVELOPING SEED;
RA Chopra V.L.;
RT "Trangenic indian mustard high in oleate.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ313331; CAC44792.1; -.
DR InterPro; IPR005067; FA_desat.
DR Pfam; PF03405; FA_desaturase.2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; UNKNOWN1.
SQ SEQUENCE 396 AA; 45054 MW; 4945DFAC6687BEB2 CRC64;

Query Match 91.1%; Score 1746; DB 10; Length 396;
Best Local Similarity 89.8%; Pred. No. 8.5e-135;
Matches 326; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 1 ASTLKSQKEVENLKKPMPREHVQVTHSMPPQKIEFKSLDWAENILVHLKPVKEK 60
DB 34 ASTLSSGKEVETVKRPNPPREHVQVTHSMPPQKIEFKALDMDADNNILVHLKPVKEK 93
QY 61 CWPQDFLPDPSGDFDQVRELREAKEIPDDYFVVLGDMITEALPTQYTMNTLDG 120
DB 94 CWPQDFLPDPSGDFDQVRELREAKEIPDDYFVVLGDMITEALPTQYTMNTLDG 153
QY 121 VRDETGAAPTSAIWTAWTAENRHGDLNKKYLSGRVDMRQIEKTIQYLGSGMDPR 180
DB 154 VRDETGAAPTSAIWTAWTAENRHGDLNKKYLSGRVDMRPNKGFYRIGSGMDPR 213
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDILKLAQICGTAADEKRHETAYTKIV 240
DB 214 TENSPLYGFIYTSFOERATFISHGNTARLAREHGDILKLAQICGTAADEKRHETAYTKIV 273
QY 241 EKLFEIDPDGTVLAFADMMRKKSIPAHLMVDGRDNLFDHFSVAQRLGVYTKADYADI 300
DB 274 EKLFEIDPDVTVLAFADMMRKKSIPAHLMVDGRDNLFDHFSVAQRLGVYTKADYADI 333
QY 301 LEFLVGRMKVKDLTGLSAGQKAQDYVCLPPIRRLEERAQRAKEAPTMPFIFDRQ 360
DB 334 LEHLVARNKVANLTGLSADGQKAQDYVCGLPPIRRLEERAQRAKAPKIPFSWVHRE 393
QY 361 VKL 363
DB 394 VOL 396

RESULT 4
O22832
ID O22832 PRELIMINARY; PRT; 401 AA.
AC O22832;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
DE desaturase).
GN AT2G43710 OR SS12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=21374454; PubMed=11481500;
RA Kachroo P., Shanklin J., Shah J., Whittle E.J., Klessig D.F.;
RT "A fatty acid desaturase modulates the activation of defense signaling
RT pathways in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9448-9453(2001).
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL; AC002333; AAB64035.1; -.
DR EMBL; AF395441; AAK85232.1; -.
DR HSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR01225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase.2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 401 AA; 45693 MW; 0C46984578D4E1D1 CRC64;

Query Match 90.4%; Score 1733; DB 10; Length 401;
Best Local Similarity 89.4%; Pred. No. 1e-133;
Matches 322; Conservative 22; Mismatches 16; Indels 0; Gaps 0;

QY 4 LKSGSKEVENLKKPMPREHVQVTHSMPPQKIEFKSLDWAENILVHLKPVKEKWQ 63
DB 42 LSSGPKVESEKPKPTPPREHVQVTHSMPPQKIEFKSMENWAEENLLIHLKDVESWQ 101
QY 64 PODELPDPSGDFDQVRELREAKEIPDDYFVVLGDMITEALPTQYTMNTLDGVRD 123
DB 102 PODELPDPSGDFDQVRELREAKEIPDDYFVVLGDMITEALPTQYTMNTLDGVRD 161
QY 124 ETGASPTSAIWTAWTAENRHGDLNKKYLSGRVDMRQIEKTIQYLGSGMDPRTEN 183
DB 162 ETGASPTSAIWTAWTAENRHGDLNKKYLSGRVDMRQIEKTIQYLGSGMDPRTEN 221
QY 184 SPYLGFIYTSFOERATFISHGNTARQAKEHGDILKLAQICGTAADEKRHETAYTKIVEKL 243
DB 222 NPYLGIYTSFOERATFISHGNTARQAKEHGDILKLAQICGTAADEKRHETAYTKIVEKL 281
QY 244 FEIDPDGTVLAFADMMRKKSIPAHLMVDGRDNLFDHFSVAQRLGVYTKADYADILEF 303
DB 282 FEIDPDGTVMFAFADMMRKKSIPAHLMVDGRDNLFDHFSVAQRLGVYTKADYADILEF 341
QY 304 LVGRMKVKDLTGLSAGQKAQDYVCLPPIRRLEERAQRAKEAPTMPFIFDRQVKL 363
DB 342 LVGRMKIQLTGLSGENKAQDYVCLPPIRRLEERAQRAKAPKIPFSWIHREVQL 401

RESULT 5
Q94AE9
ID Q94AE9 PRELIMINARY; PRT; 401 AA.
AC Q94AE9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE At2g43710/F18019.18.
```

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.-M., Lin J.,
RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048233; AK82496.1; -
DR EMBL; AY040414; AA016170.1; -
DR InterPro; IPR005067; FA.desat.
-DR InterPro; IPR001225; FA.desaturase.2;
DR Pfam; PF03405; FA.desaturase.2; 1.
DR PROSITE; PS00574; FATTY-ACID-DESATURASE; 1.
DR SC PROSITE; 401 AA; 45692 MW; 01F09DD370F4E1D1_CRC64;

Query Match	90.2%	Score 1729;	DB 10;	Length 401;
Best Local Similarity	89.2%;	Pred. No. 2.2e-133;		
Matches 321;	Conservative 23;	Mismatches 16;	Indels 0;	Gaps 0;

Qy	4	LKSGSKEVENLKPFMPPREVHVQVTHSWPQKTEIFKSLONWAEENTLVHLKPVEKCWQ	63
Db	42	LSSGPEKVESLKPPPPREHVQVHLHWPQKTEIFKSMENWAEENLLIHLKDVKEKSW	101
Qy	64	PODFLPDPASDGFQDQRELREARKEIPDDYFVVLVGDMMITEALPTYQTMLNTLDGVRD	123
Db	102	PODFLPDPASDGFQDQRELREARERELPDDYFVVLVGDMMITEALPTYQTMLNTLDGVRD	161
Qy	124	ETGASPTSWAIWTRAWTAENRHGDLINKLYLSGRVDMRQIEKTIQVILGSGMDPRTEN	183
Db	162	ETGASPTSWAIWTRAWTAENRHGDLINKLYLSGRVDMRQIEKTIQVILGSGMDPRTEN	221
Qy	184	SPYLGFIYTSFOERATFTSHGNTARQAEHGDIKLAQICGTIAADEKKRHETAYTKIVEKL	243
Db	222	NPYLGFIYTSFOERATFTSHGNTARQAEHGDIKLAQICGTIAADEKKRHETAYTKIVEKL	281
Qy	244	FEIDPDGTVLAFADMMRKISKIMPAHLMYDGRDNLFDHFSVAQAQLGVYVYAKDYADILEF	303
Db	282	FEIDPDGTVMAPADMMRKISKIMPAHLMYDGRDNLFDNFSSVAQAQLGVYVYAKDYADILEF	341
Qy	304	LVGRWKVKDLTGLSRAEQAKADYVVCRLPPRIRLREERAGRAKEAPTWPFSWIFDROVKL	363
Db	342	LVGRWKIKODLTGLSGEGNKADYLCGLAPRIKRLDERAQARAKGPKIPFSWIHDREVQL	401

RESULT 6
O24497
ID O24497
AC O24497;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
 DE desaturase).
 DE Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Helianthus.
 OC NCBI_TaxID=4232;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MAMMOTH;
 RA Hongtrakul V., Slabaugh M.B., Knapp S.J.;;
 RC "Sunflower stearoyl-ACP desaturase."
 RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RL -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CC CHAIN (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
 CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
 CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
 CC SIMILARITY).
 CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 CC OILS.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 DR EMBL; U91339; AAB65144.1; -.
 DR HSSP; P22337; IAFR.
 DR InterPro; IPR005067; FA_desat.
 DR InterPro; IPR001225; FA_desaturase.
 DR Pfam; PF03405; FA_desaturase_2; 1.
 DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
 DR DR Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
 KW Transít peptide.
 SK SEQUENCE 396 AA; 45128 MW; BC79CA9631952E11 CRC64;
 SQ

[illegible]

O24498;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ACyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAMMOTH;
RA Hongtrakul V., Slabaugh M.B., Knapp S.J.;
RL "Sunflower stearoyl-ACP desaturase.";
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL; U91340; AAB65145.1; -;
DR HSSP; P22337; 1A9R.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 396 AA; 45112 MW; C9D88CD04310BBFA CRC64;

Query Match 88.8%; Score 1701; DB 10; Length 396;
Best Local Similarity 88.4%; Pred. No. 4.2e-131;
Matches 321; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ASTLKSQSGKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 34 ASTIGSATTKVSTKKPTPPREVHQVQLHSMPPQKIEIFKSMGWAEDNLLVHLKPVEK 93

Qy 61 CWPQDFLPDPASDGFDEQVRELRRARAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 120
Db 94 CWPQDFLPDPASDGFMEQVEELRRARAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 153

Qy 121 VRDETGAAPTSMWAIWTRAWTAENRHGDLNLYLSGRVDNRQTEKTIQYLLIGSGMDPR 180
Db 154 VRDETGAAPTSMWAIWTRAWTAENRHGDLNLYLSGRVDNRQTEKTIQYLLIGSGMDPR 213

Qy 181 TENSPLYGLFIYTSFOERATFISHGNTARAKHEGDIKLAQICGTIAADEKRHETATYTKIV 240
Db 214 TENSPLYGLFIYTSFOERATFISHGNTARAKHEGDIKLAQICGTIAADEKRHETATYTKIV 273

Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSVAQRLGVYTKADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSVAQRLGVYTKADYADI 333

Qy 301 LEFLVGRWKVKDLTGLSAGEQKADYVCLPPIRRLEERAQGRAKEAPTFPFSWIFDRQ 360
Db 334 LEFLVGRWKVKDLTGLSAGEQKADYVCLPPIRRLEERAQGRAKEAPTFPFSWIFDRQ 393

Qy 361 VKL 363
Db 394 VKL 396

RESULT 8
Q9SEK6
ID Q9SEK6 PRELIMINARY; PRT; 396 AA.
AC Q9SEK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ACyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Persea americana (Avocado).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
OX NCBI_TaxID=3435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. FUERTE;
RA Madi L., Prusky D.;
RT "Sequence of a cDNA Clone Encoding an Avocado (Persea americana) [delta9]- Stearoyl-Acyl Carrier Protein Desaturase (Accession No. AF116861). (PCR99-167).";
RL Plant Physiol. 121:1054-1054(1999).
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL; AF116861; AAF15308.1; -;
DR HSSP; P22337; 1A9R.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 396 AA; 45454 MW; 0F971ABDC07C2AD7 CRC64;

Query Match 88.6%; Score 1698; DB 10; Length 396;
Best Local Similarity 87.1%; Pred. No. 7.3e-131;
Matches 316; Conservative 27; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ASTLKSQSGKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 34 ASTLSSQSGKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93

Qy 61 CWPQDFLPDPASDGFDEQVRELRRARAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 120
Db 94 CWPQDFLPDPASDGFESVEELRRARAKEIPDEYFVCLVGMITEALPTYQTMNTLDG 153

Qy 121 VRDETGAAPTSMWAIWTRAWTAENRHGDLNLYLSGRVDNRQTEKTIQYLLIGSGMDPR 180
Db 154 VRDETGAAPTSMWAIWTRAWTAENRHGDLNLYLSGRVDNRQTEKTIQYLLIGSGMDPR 213

Qy 181 TENSPLYGLFIYTSFOERATFISHGNTARAKHEGDIKLAQICGTIAADEKRHETATYTKIV 240
Db 214 TENSPLYGLFIYTSFOERATFISHGNTARAKHEGDIKLAQICGTIAADEKRHETATYTKIV 273

Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSVAQRLGVYTKADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSVAQRLGVYTKADYADI 333

Qy 301 LEFLVGRWKVKDLTGLSAGEQKADYVCLPPIRRLEERAQGRAKEAPTFPFSWIFDRQ 360
Db 334 LEFLVRRMDVEHLTGLSPGKTAQEFICKLAPRIRSLERARSRAKEGPTIPFSWIFNRE 393

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Qy 361 VKL 363
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Db 394 VKL 396

RESULT 9
Q39355 PRELIMINARY; PRT; 401 AA.
ID Q39355 AC Q39355;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (stearoyl-ACP
desaturase).
GN BNA.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. JET NEUF.
RX MEDLINE=94286739; PubMed=8016261;
RA Slocumbe S.P., Piffanelli P., Fairbairn D., Bowra S., Hatzopoulos H.,
RA T'siantis M., Murphy D.J.;
RT "Temporal and tissue specific regulation of a Brassica napus stearoyl-
acyl carrier protein desaturase gene.";
RL Plant Physiol. 104:1167-1176(1994).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
= OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL; AF172782; CAA52786.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 401 AA; 45482 MW; 1CCFBI5626270401 CRC64;

Query Match 88.6%; Score 1698; DB 10; Length 401;
Best Local Similarity 86.7%; Pred. No. 7.5e-131;
Matches 312; Conservative 30; Mismatches 18; Indels 0; Gaps 0;

Qy 4 LKSGSKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENLIVHLKPKVEKQW 63
|||
Db 42 LSSSTKEVESLKKPPTPPKEVHVQVTHSMPPQKIEIFKSLDNWAEENLIVHLKPKVEKSWQ 101
|||||
Qy 64 PDDFLPDASDGFDEQVRELRAKEIPDDYFVVLVGMNITEALPTVOTMLNTLDGVYRD 123
|||||
Db 102 PDDFLPDASDGFDEQVRELRAKEIPDDYFVVLVGMNITEALPTVOTMLNTLDGVYRD 161
|||||
Qy 124 ETGASPTSWAIVTAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPR 183
|||||
Db 162 ETGASPTSWAIVTAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPR 221
|||||
Qy 184 SPYLGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTAADEKREHETAYTKIV 243
|||||
Db 222 NPYLGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTAADEKREHETAYTKIV 281
|||||
Qy 244 FEIDPDCTVAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRILGVVYTAADYADILEF 303
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Db 282 LEIDPDCTVAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRILGVVYTAADYADILEF 341
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Qy 304 LVGRWVKDKLTGLSAGOKAODYVCLPPIRRLERAGRAKEAPMPFSLFEDROVKL 363
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Db 342 LVGRWKIESLSGLSGEGNAQEYLGLTPRIKRLDERAARAKKGPFIKPSWIHREVQL 401
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RESULT 10
Q9SW87 PRELIMINARY; PRT; 409 AA.
ID Q9SW87 AC Q9SW87;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (stearoyl-ACP
desaturase).
OS Arachis hypogaea (Peanut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;
OC Arachis.
OX NCBI_TaxID=3818;
RN [1]
RP SEQUENCE FROM N.A.
RA Tate P.L., Kochert G., Abbott A.G.;
RT "The phylogenetic relationship of the cultivated peanut (Arachis
hypogaea L.) to its wild relative based upon comparisons of stearoyl-
ACP desaturase sequences.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
= OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL; AF172728; AAD48495.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 409 AA; 46810 MW; 7C80926BD8534A58 CRC64;

Query Match 88.5%; Score 1696.5; DB 10; Length 409;
Best Local Similarity 87.2%; Pred. No. 1e-130;
Matches 319; Conservative 24; Mismatches 20; Indels 3; Gaps 1;

Qy 1 ASTLKSKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENLIVHLKPKVEK 60
|||||
Db 44 ASTLTSKEVENLKKPPTPPKEVHVQVTHSMPPQKIEIFKSLDNWAEENLIVHLKPKVEK 103
|||||
Qy 61 CQWQDFLPDASDGFDEQVRELRAKEIPDDYFVVLVGMNITEALPTVOTMLNTLDG 120
|||||
Db 104 CQWQDFLPDASDGFDEQVRELRAKEIPDDYFVVLVGMNITEALPTVOTMLNTLDG 163
|||||
Qy 121 VRDETASPTSWAIVTAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPR 180
|||||
Db 164 VRDETASPTSWAIVTAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPR 223
|||||
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTAADEKREHETAYTKIV 240
|||||
Db 224 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTAADEKREHETAYTKIV 283
|||||
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Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADI 300
 Db 284 EKLFEIDPDGTVMAFADMMRKKIAMPAHLMYDGRDNLDFENYSAVAQRIGVYTKADYADI 343
 Qy 301 LEFLVGRWKVDKLTGLSNEGOKAODYVCRLLP---RIRRLERAGRAKEAPTWPFSWIF 357
 Db 344 LEFLVARKVADLTGLSGEGRKAODYVCRCPRIIRRLERAGRAKESPRLKFSWIY 403
 Qy 358 DROVKL 363
 Db 404 DREVQL 409

RESULT 11
 Q9XQR7
 ID Q9XQR7 PRELIMINARY; PRT; 401 AA.
 AC Q9XQR7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 DE FAB2.
 GN Brassica juncea (Leaf mustard) (Indian mustard).
 OS Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3707;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PUSA JAIKISAN;
 RA Vageshbabu H.S., Kirti P.B., Chopra V.L.;
 RT "Nucleotide sequence of the coding region of the plastidic delta-9-stearoyl-acyl carrier protein desaturase of Brassica juncea.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACRYL CHAIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 DR EMBL; AF153420; AAD40245.1; -.
 DR HSP; P22337; IAFR.
 DR InterPro; IPR005067; FA_desat.
 DR InterPro; IPR001225; FA_desaturase.
 DR Pfam; PF03405; FA_desaturase_2; 1.
 DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
 DR Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; Transit peptide.
 KW Transit peptide.
 SQ SEQUENCE 401 AA; 45504 MW; 1726DA429DCF00EB CRC64;

Query Match 88.5%; Score 1695; DB 8; Length 401;
 Best Local Similarity 86.4%; Pred. No. 1.3e-130;
 Matches 311; Conservative 30; Mismatches 19; Indels 0; Gaps 0;

Qy 4 LKSGSKEVENLKPKMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVKQW 63
 Db 42 LSSSTKEVESLKKPPTPPKREHVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVKQW 101
 Qy 64 PQDFLPDPASGDFGVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMINTLDGVRD 123
 Db 102 PQDFLPDPASGDFGVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMINTLDGVRD 161
 Qy 124 ETGASPTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYLGSGMDPRPTEN 183

Db 162 ETGASPTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYLGSGMDPRPTEN 221
 Qy 184 SPYLGFIYTSQERATFISHGNTARAKEHGDILKLAQICGTAADKREHETAYTKIVEKL 243
 Db 222 NPYLGFYITSQERATFVSHGNTARAKEHGDILKLAQICGTAADKREHETAYTKIVEKL 281
 Qy 244 FEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADILEF 303
 Db 282 LEIDPDGTVVAFADMMRKKISMPAHLMYDGRDNLDFNFSVAQRLGVYTKADYADILEF 341
 Qy 304 LVGRWKVDKLTGLSNEGOKAODYVCRLLPPIRRLERAGRAKEAPTWPFSWIFRQVKL 363
 Db 342 LAGRWKIESLSGEGNKAQEYLCGLTPRIIRRLDERAQAARAKGPKIPFWSIHREYQL 401

RESULT 12

O65040
 ID O65040 PRELIMINARY; PRT; 396 AA.
 AC O65040;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 DE FAD1.
 GN Macfadyena unguis-cati.
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Bignoniaceae; Macfadyena.
 OX NCBI_TaxID=73871;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cahoon E.B., Shah S., Shanklin J., Browse J.;
 RT "A Determinant of Substrate Specificity Predicted from the Acyl-ACP Desaturase of Developing Doxantha Seed.";
 RL Plant Physiol. 0:0-0(1998).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACRYL CHAIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 DR EMBL; AF051134; AAC05293.1; -.
 DR HSP; P22337; IAFR.
 DR InterPro; IPR005067; FA_desat.
 DR InterPro; IPR001225; FA_desaturase.
 DR Pfam; PF03405; FA_desaturase_2; 1.
 DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
 DR Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; Transit peptide.
 KW Transit peptide.
 SQ SEQUENCE 396 AA; 45231 MW; 0101A75855605C57 CRC64; 1

Query Match 88.1%; Score 1688; DB 10; Length 396;
 Best Local Similarity 87.3%; Pred. No. 4.8e-130;
 Matches 317; Conservative 24; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ASTLKSKEVENLKPKMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 60
 Db 34 AATLSGRUDVTKKTFSPAREHVHVQVTHSMAPQKIEFKRAMEDWANNILVHLKNVEK 93
 Qy 61 CWQDFLPDPASGDFGVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMINTLDG 120
 Db 94 CPQDFLPDPASGDFGVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMINTLDG 153
 Qy 121 VRDETASPTSWAIWTRAWTAENRHGDLNKLKYLGRVDMRQIEKTIQYLGSGMDPR 180


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Db 154 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDITKLAQICGTIAADEKRHETATYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARLARDHGDFKLAQICGTIASDEKRHETATYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 333
Qy 301 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLLEERAQRAKEAPTMPSWIFDRQ 360
Db 334 LEHLVGRWKVEKLTGLSAGGKAQDYVCGLPPIRRLLEERAQIRAKQAPRLPFSWIDRE 393
Qy 361 VKL 363
Db 394 VQL 396

RESULT 13
Q8VXJ7 PRELIMINARY; PRT; 396 AA.
AC Q8VXJ7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Stearoyl-ACP desaturase I (EC 1.14.99.6).
GN SDSL.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN SEQUENCE FROM N.A.
RP STRAIN=CAS-8;
RT Martinez-Force E., Fernandez-Moya V., Garces R.;
RL "Stearoyl-ACP desaturases in high-stearic sunflower mutants.";
DR EMBL; AJ242632; CAC80360.1; -
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; UNKNOWN_1.
KW Oxidoreductase.
OX NCBI_TaxID=4232;
RN SEQUENCE FROM N.A.
RP STRAIN=CAS-8;
RT Martinez-Force E., Fernandez-Moya V., Garces R.;
RL "Stearoyl-ACP desaturases in high-stearic sunflower mutants.";
DR EMBL; AJ242632; CAC80360.1; -
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 396 AA; 45087 MW; F439BA366C4EB211 CRC64;

Query Match 87.3%; Score 1673; DB 10; Length 396;
Best Local Similarity 87.1%; Pred. No. 8.2e-129;
Matches 316; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENLVLHKPVEK 60
Db 34 ASTIGSATTKVESTKPKFTPPREVHQVQLHSMPPQKIEIFKSGEWAEDNLVLHKPVEK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTYQTMLNTLDG 120
Db 94 CWAQDFLPDPASDGFMEQVELRAKEIPDDYFVVLVGMITEEALPTYQTMLNTLDG 153
Qy 121 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 180
Db 154 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDITKLAQICGTIAADEKRHETATYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARHAKHGVDKLAQMGCIIAADEKRHETATYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 333
Qy 301 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLLEERAQRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVDKLTGLSAGGKAQDYVCGLPPIRRLLEERAQIRAKQAPRLPFSWIDRE 393
Qy 361 VKL 363
Db 394 VQL 396

RESULT 15
Q42591 PRELIMINARY; PRT; 407 AA.
ID Q42591
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Db 334 LEFLVGRWKVDKLTGLSAGGKAQDYVCGLPPIRRLLEERNSARAKERNVVPFSWLDRE 393
Qy 361 VKL 363
Db 394 VQL 396

RESULT 14
Q8VXJ8 PRELIMINARY; PRT; 396 AA.
AC Q8VXJ8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Stearoyl-ACP desaturase I (EC 1.14.99.6).
GN SDSL.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN SEQUENCE FROM N.A.
RP STRAIN=CAS-4;
RT Martinez-Force E., Fernandez-Moya V., Garces R.;
RL "Stearoyl-ACP desaturases in high-stearic sunflower mutants.";
DR EMBL; AJ242631; CAC80359.1; -
DR Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 396 AA; 45062 MW; 2E4C366839EBB347 CRC64;

Query Match 87.2%; Score 1670; DB 10; Length 396;
Best Local Similarity 87.1%; Pred. No. 1.4e-128;
Matches 316; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENLVLHKPVEK 60
Db 34 ASTIGSATTKVESTKPKFTPPREVHQVQLHSMPPQKIEIFKSGEWAEDNLVLHKPVEK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTYQTMLNTLDG 120
Db 94 CWAQDFLPDPASDGFMEQVELRAKEIPDDYFVVLVGMITEEALPTYQTMLNTLDG 153
Qy 121 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 180
Db 154 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLILSGRVDMPKQIEKTIQYILIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDITKLAQICGTIAADEKRHETATYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARHAKHGVDKLAQMGCIIAADEKRHETATYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYTAADYADI 333
Qy 301 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLLEERAQRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVDKLTGLSAGGKAQDYVCGLPPIRRLLEERNSARAKERNVVPFSWXLNRE 393
Qy 361 VKL 363
Db 394 VQL 396

RESULT 15
Q42591 PRELIMINARY; PRT; 407 AA.
ID Q42591
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AC Q42591;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
DE desaturase).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ANIMAL PARTS;
RA Piffanelli P., Murphy D.J.;
RT "Cloning of a stearyl-ACP desaturase from Arabidopsis thaliana.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACRYL
CC CHAIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL; X93461; CAA63746.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW transit peptide.
SQ SEQUENCE 407 AA; 46102 MW; 8235B14908442C96 CRC64;

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Query Match 86.7%; Score 1660.5; DB 10; Length 407;
Best Local Similarity 87.9%; Pred. No. 9e-128;
Matches 31; Conservative 21; Mismatches 17; Indels 5; Gaps 1;

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QY 4 LKSGSKEVENLKPPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVCKWQ 63
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Db 42 LSSGPEVESLKKPTPPREHVHVQVLSHMPQKIEIFKSMENWAEENLLIHLKOVESWQ 101
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 64 PQDFLPDPASGDFEQVRELREAKEIPDDYFVVLVGDNITEALPTYOTMLNTLDGVRD 123
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 102 PQDFLPDPASGDFEQVRELREARLDDYFVVLVGDNITEALPTYOTMLNTLDGVRD 161
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 124 ETGASPTSWAIWTRAWTAENRPHGDLNKLKLYLSGRVDMRQIEKTIQYLGSGMDPRTEN 183
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 162 ETGASPTSWAIWTRAWTAENRPHGDLNKLKLYLSGRVDMRQIEKTIQYLGSGMDPRTEN 221
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 184 SPYLGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKL 243
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 222 NPYLGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKL 281
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 244 FEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRGLGYTTAKDYADILEF 303
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 282 FEIDPDGTVMAFADMMRKKISMPAHLMYDGDNDLFDNFSSVAQRGLGYTTAKDYADILEF 341
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 304 LVGRWKVDKLGSLREGOKAQDYVCRLLPPIRRLEERAQGRAK-----EAPTMP 352
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 342 LVGRWKIQDLTGLSGEGNAQDYLCGLAPRIKRLDERAQAQAKLKGQKPILP 395
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Search completed: March 7, 2003, 03:09:56
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:04:12 ; Search time 13 Seconds
(without alignments)
1158.147 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSGSREVENLKKPFMP.....RAKEAPMPFSWIFDRQVKL 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1916	100.0	396	1	STAD_RICCO
2	1764	92.1	396	1	STAD_CUCSA
3	1752	91.4	396	1	STAD_CARTNI
4	1738	90.7	411	1	STAD_SOYBN
5	1724.5	90.0	399	1	STAD_SPTOL
6	1698	88.6	398	1	STAD_SPTOL
7	1680	87.7	399	1	STAD_BRANA
8	1662.5	86.8	393	1	STAD_ELAGV
9	1655	86.4	396	1	STAD_HELAN
10	1652	86.2	393	1	STAD_SOLCO
11	1649	86.1	390	1	STAD_OLLEU
12	1626	84.9	393	1	STAD_SOLTU
13	1610.5	84.1	397	1	STAD_GOSHI
14	1607	83.9	398	1	STAD_SIMCH
15	1583	82.6	390	1	STAD_ORYSA
16	1465	76.5	396	1	STAD_LINUS
17	1317	68.7	385	1	STAD_CORSA
18	104.5	5.5	665	1	TKT_BUCAT
19	101.5	5.3	3421	1	TEGU_HSVBB
20	101	5.3	1188	1	S3B1_SCHPO
21	99.5	5.2	375	1	RIR2_ECOLI
22	98.5	5.1	1304	1	S3B1_HUMAN
23	98.5	5.1	1304	1	S3B1_MOUSE
24	98.5	5.1	1307	1	S3B1_XENLA
25	97.5	5.1	449	1	YBB9_SCHPO
26	97	5.1	820	1	SYL_CHLPN
27	97	5.1	2096	1	BP28_DROME
28	96.5	5.0	709	1	PNP_PHOLU
29	96	5.0	858	1	ALR2_YEAST
30	95.5	5.0	375	1	RIR2_SALTY
31	93.5	4.9	643	1	NOS3_ALCEU
32	93.5	4.9	671	1	VINE_HUMAN
33	92.5	4.8	578	1	YBX6_SCHPO

RESULT 1

ID	STAD_RICCO	STANDARD;	PRT;	396 AA.
AC	P22337;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Acyl-[acyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase) (Delta(9) stearoyl-acyl carrier protein desaturase).			
DE	Ricinus communis (Castor bean).			
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid I; Malpighiales; Euphorbiales; Ricinus.			
OC	NCBI_TaxID=3988;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91172837; PubMed=2006187;			
RA	Shanklin J., Somerville C.R.;			
RT	"Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally unrelated to the animal and fungal homologs.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Endosperm;			
RA	Knutzon D.S., Scherer D.E., Schreckengost W.E.;			
RT	"Nucleotide sequence of a complementary DNA clone encoding stearoyl-acyl carrier protein desaturase from castor bean, Ricinus communis.";			
RL	Plant Physiol. 96:344-345(1991).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).			
RX	MEDLINE=97015109; PubMed=8861937;			
RA	Lindqvist Y., Huang W., Schneider G., Shanklin J.;			
RT	"Crystal structure of delta9 stearoyl-acyl carrier protein desaturase from castor seed and its relationship to other di-iron proteins.";			
RL	EMBO J. 15:4081-4092(1996).			
CC	!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACRYL CHAIN.			
CC	!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2) = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.			
CC	!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.			
CC	!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.			
CC	!- SUBUNIT: HOMODIMER.			
CC	!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES.			
CC	!- TISSUE SPECIFICITY: HIGHER LEVELS IN DEVELOPING SEEDS THAN IN LEAF AND ROOT TISSUES.			
CC	!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way			

Q04322 saccharomyc
Q43848 solanum tub
Q12955 homo sapien
Q9wlm8 drosophila
Q9ka72 bacillus ha
Q03585 thermoplas
Q10592 mycobacteri
Q57775 methanococc
P13267 bacillus su
P56142 helicobacte
P45825 mycobacteri
P08032 mus musculu

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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL; M59857; AAA74692.1; ALT_INIT.
 DR EMBL; X56508; CAA39859.1; -
 DR PIR; S16463; OHCSAD.
 DR PIR; A39170; A39170.
 DR PDB; IAFR; 15-MAY-97.
 DR InterPro; IPR005067; FA_desat.
 DR InterPro; IPR001225; FA_desaturase.
 DR Pfam; PF03405; FA_desaturase.2; 1.
 DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
 KW Transit peptide; 3D-structure.
 FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 34 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
 SQ SEQUENCE 396 AA; 45371 MW; E50D4725996392AF CRC64;

Query Match 100.0%; Score 1916; DB 1; Length 396;
 Best Local Similarity 100.0%; Pred. No. 2e-140;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVK 60
 DB 34 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVK 93
 QY 61 CWQPDPLPDPSADGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 120
 DB 94 CWQPDPLPDPSADGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 153
 QY 121 VRDETASPTSWAIWTRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTIQYLLGSGMDPR 180
 DB 154 VRDETASPTSWAIWTRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTIQYLLGSGMDPR 213
 QY 181 TENSPLYGLFYTSFQERATFISGNTARQAKHEGDKLQAOICGTIAADKRKHETATYKIV 240
 DB 214 TENSPLYGLFYTSFQERATFISGNTARQAKHEGDKLQAOICGTIAADKRKHETATYKIV 273
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYAKDYADI 300
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYAKDYADI 333
 QY 301 LEFLVGRWKVDKLTGLSAEGQKADQYVCRLLPPIRRLEERAQRAKEAPTMPSWIFDRQ 360
 DB 334 LEFLVGRWKVDKLTGLSAEGQKADQYVCRLLPPIRRLEERAQRAKEAPTMPSWIFDRQ 393
 QY 361 VKL 363
 DB 394 VKL 396

RESULT 2
 STAD_CUCSA STANDARD; PRT; 396 AA.
 ID STAD_CUCSA
 AC P32061;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Cucumis sativus (Cucumber).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 OX NCBI_TaxID=3659;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seedling cotyledon;
 RA Shanklin J., Mullins C., Somerville C.R.;
 RT "Sequence of a complementary DNA from Cucumis sativus L. encoding the
 RT* stearoyl-acyl-carrier protein desaturase."
 RL Plant Physiol. 97:467-468(1991).

RN SEQUENCE FROM N.A.
 RP MEDLINE=91172837; PubMed=2006187;
 RX Shanklin J., Somerville C.;
 RA "Stearoyl-acyl-carrier-protein desaturase from higher plants is
 RT structurally unrelated to the animal and fungal homologs."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).
 CC !- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CC CHAIN.
 CC !- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O
 CC !- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC !- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 CC OILS.
 CC !- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC !- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
 CC NONPHOTOSYNTHETIC TISSUES.
 CC !- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M59858; AAA33130.1; -
 DR PIR; B39170; B39170.
 DR HSP; P22337; IAFR.
 DR InterPro; IPR005067; FA_desat.
 DR InterPro; IPR001225; FA_desaturase.
 DR Pfam; PF03405; FA_desaturase.2; 1.
 DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
 KW Transit peptide.
 FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 34 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
 FT CONFLICT 114 114 R -> V (IN REF. 2).
 FT CONFLICT 290 290 E -> D (IN REF. 2).
 SQ SEQUENCE 396 AA; 45583 MW; 2E19E894C106D4C8 CRC64;
 Query Match 92.1%; Score 1764; DB 1; Length 396;
 Best Local Similarity 90.4%; Pred. No. 1e-128;
 Matches 328; Conservative 20; Mismatches 15; Indels 0; Gaps 0;
 QY 1 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVK 60
 DB 34 ASTLKSGSKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVK 93
 QY 61 CWQPDPLPDPSADGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 120
 DB 94 CWQPDPLPDPSADGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 153
 QY 121 VRDETASPTSWAIWTRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTIQYLLGSGMDPR 180
 DB 154 VRDETASPTSWAIWTRAWTAENRRHGDLLNKLYLSGRVDMRQIEKTIQYLLGSGMDPR 213
 QY 181 TENSPLYGLFYTSFQERATFISGNTARQAKHEGDKLQAOICGTIAADKRKHETATYKIV 240
 DB 214 TENSPLYGLFYTSFQERATFISGNTARQAKHEGDKLQAOICGTIAADKRKHETATYKIV 273
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYAKDYADI 300
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGVYAKDYADI 333
 QY 301 LEFLVGRWKVDKLTGLSAEGQKADQYVCRLLPPIRRLEERAQRAKEAPTMPSWIFDRQ 360
 DB 334 LEFLVGRWKVDKLTGLSAEGQKADQYVCRLLPPIRRLEERAQRAKEAPTMPSWIFDRQ 393
 QY 361 VKL 363


```
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 28 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 29 411 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 411 AA; 47282 MW; 2727C3BDC8C97BA8 CRC64;

Query Match 90.7%; Score 1738; DB 1; Length 411;
Best Local Similarity 89.4%; Pred. No. 1.1e-126;
Matches 322; Conservative 25; Mismatches 13; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 60
DB 29 ASTLSSGSKEVENLKPPMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 88
QY 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMLTEALPTYOTMLNTLDG 120
DB 89 CWPQDFLPDPSSDGFDEQVRELRAKEIPDDYFVVLVGDMLTEALPTYOTMLNTLDG 148
QY 121 VRDETGAISPTSWAITWRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
DB 149 VRDETGAISPTSWAITWRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 208
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDKIKLAQICGTIAADEKRKHETATYKIV 240
DB 209 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDKIKLAQICGTIAADEKRKHETATYKIV 268
QY 241 EKLFEPDGTGLAFADMMRKKSMPAHLMYDGRDNLDFHESAVAQRLGVYTAQYADI 300
DB 269 EKLFESPDGTGLAFADMMRKKSMPAHLMYDGRDNLDFHESAVAQRLGVYTAQYADI 328
QY 301 LEFLVGRWKVKDKLTGLSAEGQAKQADYVCLPPIRRLEERAQRAKEAPTMPFSWIFDR 360
DB 329 LEFLVGRWKVKDKLTGLSGEGRKAQYICGLPPIRRLEERAQRAKEAPTMPFSWIFDR 388

RESULT 5
- STAD_SP10L STANDARD; PRT; 399 AA.
AC P28645;
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ACYL-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bifolia; TISSUE=Cotyledon;
RX MEDLINE=92329733; PubMed=1627785;
RA Beppu T., Nishida I., Matsuo T., Murata N.;
RT "Nucleotide sequence of a cDNA clone encoding a precursor to
RT stearyl-(acyl-carrier-protein) desaturase from spinach, Spinacia
RT oleracea."
RL Plant Mol. Biol. 19:711-713(1992).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X62898; CAA44687.1; -.
CC PIR; S22480; OHSPAD.
CC HSSP; P22337; 1AFR.
CC InterPro; IPR005067; FA_desat.
CC InterPro; IPR001225; FA_desaturase.
CC Pfam; PF03405; FA_desaturase_2; 1.
CC PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 35 CHLOROPLAST.
FT CHAIN 36 399 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 399 AA; 45663 MW; 59B56E0609EA7CCC CRC64;

Query Match 90.0%; Score 1724.5; DB 1; Length 399;
Best Local Similarity 87.9%; Pred. No. 1.1e-125;
Matches 320; Conservative 27; Mismatches 16; Indels 1; Gaps 1;

QY 1 ASTLKSGS-KEVENLKPPMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 59
DB 36 ASTLSSSGSKEVENLKPPMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVK 95
QY 60 KCWQPDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMLTEALPTYOTMLNTLD 119
DB 96 KCWQPDFLPDPASEDFRDOVKIEQRAKEIPDDLYVLVGDMLTEALPTYOTMLNTLD 155
QY 120 GVRDETGAISPTSWAITWRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDP 179
DB 156 GAKDETGAISPTSWAITWRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDP 215
QY 180 RTENSPLYGFIYTSFQERATFISHGNTARQAKHEGDKIKLAQICGTIAADEKRKHETATYKI 239
DB 216 RTENNPYLGFIYTSFQERATFVSHGNSARLAKHEGDLKMAQICGTIASDEKRKHETATYKI 275
QY 240 VEKLFEPDGTGLAFADMMRKKSMPAHLMYDGRDNLDFHESAVAQRLGVYTAQYADI 299
DB 276 VEKLFEPDGTGLAFADMMRKKSMPAHLMYDGRDNLDFHESAVAQRLGVYTAQYADI 335
QY 300 LEFLVGRWKVKDKLTGLSAEGQAKQADYVCLPPIRRLEERAQRAKEAPTMPFSWIFDR 359
DB 336 LEFLVGRWKVKDKLTGLSGEGRKAQYICGLPPIRRLEERAQRAKEAPTMPFSWIFDR 395
QY 360 QVKL 363
DB 396 QVKL 399

RESULT 6
- STAD_BRANA STANDARD; PRT; 398 AA.
AC P29108;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ACYL-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. R500;
RX MEDLINE=92212881; PubMed=1557366;
RA Knutzon D.S., Thompson G.A., Radke S.E., Johnson W.B., Knauf V.C.,
RA Kridel J.C.;
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SQ		SEQUENCE	393 AA;	44857 MW;	C6A87B8BB0D8A0CC	CRC64;	.
		Query Match	86.8%;	Score 1662.5;	DB 1;	Length 393;	
		Best Local Similarity	85.7%;	Pred. NO. 6.7e-121;			
		Matches 311;	Conservative 29;	Mismatches 22;	Indels 1;	Gaps 1;	
QY	1	ASTLKSGSKVEMLKPFMPREVHVQVTHSMPPQKEIFKSLDNWAEENILYLHLKPVEK	60				
		:					
		:					
Db	32	ASTVGSTK-V EIPKKPFMPREVHVQVTHSMPPQKEIFKSLUDWAEENILYLHLKPVEK	90				
		:					
		:					
QY	61	CWQPQDFLPDPASGDGEQVKELRERAKEIPDDYFVVVLGDMITEEALPTYQTMLNTLDG	120				
		:					
		:					
Db	91	CWQPQDFLPDPSSGEFHVEEKELRSERSKEIPDGYYVCVLGDMITEEALPTYQTMLNTLDG	150				
		:					
		:					
QY	121	VREDTGASPTSWAIWTRAWTAENNRHGDLLNKLYLSLGRVDMROIETIQYLGSGMDPR	180				
		:					
		:					
Db	151	VREDTGA SLTSWA VMTRAWTAENNRHGDLLNKLYLSLGRVDMROIETIQYLGSGMDPR	210				

Db	211	TENSPYLGFTYTSFQERATETISHGNTARHAKHEGDVRLAQTCGPTIASDEKRHETAYTKIV	270
Qy	241	EKLFEIDPDGTVLAFADMMRRKTSMPAHLMYDGRDDNLFDFHSVAORLGVYTTAKDYADI	300
		: : : : : : : : : :	
Db	271	EKLFEIDPDGTVLSFADMMRRKTSMPAHLMYDGGDDNLFDFHSVAORLGVDTAKDYADI	330
Qy	301	LEFLVGRWKYDKLTGSAEQKADQYVCRLPPIRRIRLEERAQGRAKEAPTMFWSWIFDRQ	360
Db	331	LEFLINRWKVGELTGFSGEKRAQDFVCTLAPRIIRTEERAQERAKQAPRIPCWSWIGRE	390
Qy	361	VKL 363	
Db	391	VQL 393	
RESULT 9			
	STAD_HELAN	STANDARD;	PRT; 396 AA.
AC	Q96456;		
DT	15-DEC-1998 (Rel. 37, Created)		
DT	15-DEC-1998 (Rel. 37, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Acyl-[acyl-carrier protein] desaturase, chloroplast precursor		
DE	(EC 1.14.99.6) (Stearoyl-ACP desaturase).		
OS	Helianthus annuus (Common sunflower).		
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;		
OC	Heliantheae; Helianthus.		
ON	NCBI_TaxID=4232;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. SMF3;		
RA	Coughlan S.J., Hastings C.E., Winfrey R.J.;		
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A		
CC	CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL		
CC	CHAIN.		
CC	-!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + A _h (2) + O(2)		
CC	= oleoyl-[acyl-carrier protein] + A + 2 H(2)O		
CC	-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.		
CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY		
CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE		
CC	OILS.		
CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF		
CC	NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).		
CC	-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.		
CC	-----		
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EMBL; U70374; AAB09571.1; -.
HSSP; P22337; IAFR.
InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase.2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
Transit peptide.
TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
CHAIN 34 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SEQUENCE 396 AA; 45078 MW; 97E455A116791B81 CRC64;

Query Match 86.4%; Score 1655; DB 1; Length 396;
Best Local Similarity 86.5%; Pred. No. 2.6e-120;
Matches 314; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

Qy 1 ASTLKSQSGKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 34 ASTIGSATTKVESTKKPTTPREVHVQVTHSMPPQKIEIFKSMGWAEENILVHLKPVEK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLGG 120
Db 94 CWAQDFLPDPASDGFMEQVELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLGG 153
Qy 121 VRDEGTASPTSWAINTRAWTAENRHGDLNLYLXLSGRVDMRQTEKTYQYLIGSGMDPR 180
Db 154 VRDEGTATLLGLVWTRAWTAENRHGDLNLYLXLSGRVDMRQTEKTYQYLIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKTHETATYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKTHETATYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADI 333
Qy 301 LEFLVGRWKVKDLTGLSAGQKADYVCLPRIRLEERAQGRAKEAPTMPFSWIFDRQ 360
Db 334 LEFLVGRWKVADLTGLSGEGRAQDYVCGLAPRIRLEERASARAKESVNVVPSWIFDRQ 393
Qy 361 VKL 363
Db 394 VKL 396

RESULT 10
STAD_SOLCO STANDARD; PRT; 393 AA.
ID STAD_SOLCO
AC Q41319;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Solanum commersonii (Commerçon's wild potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID:4109;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Truccini M., Grillo S., Costa A., Leone A.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.

-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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EMBL; X78935; CAA55535.1; -.
HSSP; P22337; IAFR.
InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase.2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; FALSE_NEG.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
TRANSIT 1 30 CHLOROPLAST (BY SIMILARITY).
CHAIN 31 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SEQUENCE 393 AA; 44765 MW; 5516E84FBF2C9501 CRC64;

Query Match 86.2%; Score 1652; DB 1; Length 393;
Best Local Similarity 84.8%; Pred. No. 4.3e-120;
Matches 308; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

Qy 1 ASTLKSQSGKEVENLKKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 31 ASTLPPSPVEDGNVKKPFSPREVHVQVTHSMPPKEKREIFDSLHGADNNILHGLKPVEK 90
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLGG 120
Db 91 CWAQDFLPDPASEGFDQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLGG 150
Qy 121 VRDEGTASPTSWAINTRAWTAENRHGDLNLYLXLSGRVDMRQTEKTYQYLIGSGMDPR 180
Db 151 VRDEGTASLTPWAIWTRAWTAENRHGDLNLYLXLSGRVDMRQTEKTYQYLIGSGMDPR 210
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKTHETATYTKIV 240
Db 211 TENNPHLGIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKTHETATYTKIV 270
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADI 300
Db 271 EKLFEVDPDGTVLAVADMRRKKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADI 330
Qy 301 LEFLVGRWKVKDLTGLSAGQKADYVCLPRIRLEERAQGRAKEAPTMPFSWIFDRQ 360
Db 331 LEFLVGRWEIEKLTGLSGEGHARDYVCGLAPRIRLEERAQAKQAPVPSWVFGKD 390
Qy 361 VKL 363
Db 391 VKL 393

RESULT 11
STAD_OLEEU STANDARD; PRT; 390 AA.
ID STAD_OLEEU
AC Q43593;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Olea europaea (Common olive).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Oleaceae; Olea.
OX NCBI_TaxID=4146;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Leccino; TISSUE=Mesocarp;
RA Baldoni L., Georgi L., Abbott A.G.;
RT "Nucleotide sequence of a cDNA clone from Olea europaea encoding a
RT stearyl-acyl carrier protein desaturase.";
RL (In) Plant Gene Register PGR96-052.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U58141; AAB67840.1; -.
CC HSP; P22337; IAFR.
CC InterPro; IPR005067; FA_desat.
CC Pfam; PF03405; FA_Desaturase_2; 1.
CC PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
CC Transit peptide.
CC TRANSIT 1 27 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 28 390 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
CC SEQUENCE 390 AA; 44596 MW; 39090E432B7AC2E3 CRC64;

Query Match 85.1%; Score 1649; DB 1; Length 390;
Best Local Similarity 85.1%; Pred. No. 7.3e-120;
Matches 309; Conservative 24; Mismatches 30; Indels 0; Gaps 0;

Qy 1 ASTLKSQKEVENLKKPPPPREHVQVTHSMPPQKIEFKSLDNWAEENLVHLKPVEK 60
Db 28 ASTHSPSMYGVKKPPPPREHVQVTHSLAPEKREIFNLSNNAQENLVLLKDVDR 87

Qy 61 CWPQDFLPDPSGDFEQVRELKERAKEIPDDYFVVLVGMITEEALPTQTMLNTLDG 120
Db 88 CWPQDFLPDPSGDFEQVRELKERAKEIPDDYFVVLVGMITEEALPTQTMLNTLDG 147

Qy 121 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKLYLSGRVDMROIEKTIQYLVIGSGMDPR 180
Db 148 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKLYLSGRVDMROIEKTIQYLVIGSGMDPR 207

Qy 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRIHETAYTKIV 240
Db 208 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRIHETAYTKIV 267

Qy 241 EKLFEIDPDGTVLAFADMMRKISMFAHLMYDGRDNLFDHFSVAQRLGVYTTAKDYADI 300
Db 268 EKLFEIDPDGTVLAFADMMRKISMFAHLMYDGRDNLFDHFSVAQRLGVYTTAKDYADI 327

Qy 301 LEFLVGRNWKVDTGLSREGQAQDYVCRLLPPIRRLSEERAGGRKAKEAPTFPSIFDRQ 360
Db 328 LEFLVGRNWKVDTGLSREGQAQDYVCRLLPPIRRLSEERAGGRKAKEAPTFPSIFDRQ 387

Qy 361 VKL 363

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Db 388 INL 390
RESULT 12
STAD_SOLUTU STANDARD; PRT; 393 AA.
AC P46253;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearyl-ACP desaturase).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RN SEQUENCE FROM N.A.
RA Taylor M.A., Smith S.B., Davies H.V., Burch L.R.;
RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M91238; AAA33839.1; -.
CC HSP; P22337; IAFR.
CC InterPro; IPR005067; FA_desat.
CC Pfam; PF03405; FA_Desaturase_2; 1.
CC PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
CC Transit peptide.
CC TRANSIT 1 30 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 31 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
CC SEQUENCE 393 AA; 44538 MW; 3FBCC28D57CA7FF CRC64;

Query Match 84.9%; Score 1626; DB 1; Length 393;
Best Local Similarity 82.4%; Pred. No. 4.4e-118;
Matches 299; Conservative 34; Mismatches 30; Indels 0; Gaps 0;

Qy 1 ASTLKSQKEVENLKKPPPPREHVQVTHSMPPQKIEFKSLDNWAEENLVHLKPVEK 60
Db 31 ASTHSPSMYGVKKPPPPREHVQVTHSMPPQKIEFKSLDNWAEENLVHLKPVEK 90

Qy 61 CWPQDFLPDPSGDFEQVRELKERAKEIPDDYFVVLVGMITEEALPTQTMLNTLDG 120
Db 91 CWPQDFLPDPSGDFEQVRELKERAKEIPDDYFVVLVGMITEEALPTQTMLNTLDG 150

Qy 121 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKLYLSGRVDMROIEKTIQYLVIGSGMDPR 180
Db 151 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKLYLSGRVDMROIEKTIQYLVIGSGMDPR 210

Qy 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRIHETAYTKIV 240

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Db 211 TENNPYLGEVYTSRKGVTFSHGNTARLAKHEGDMKLAQTCGTAADKKRHETAYTKIV 270
      |||:|||||:||||: ||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 241 EKLFEIDPDGTVLAFADMMRKKSIMPAHLMYDGRDDNLFDFHSVAORLGVYTAQDYADI 300
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 271 EKLLEVPDGAVALGDMRKNISMPAHLMYDGRDDNLFDFHSVAORLGVYTAQDYADI 330
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 301 LEFLVGRWKVKDLTGLSAGQKADYVCRLLPPRIRLRLEERAQRAKEAPTMPFSWIFDRQ 360
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 331 LEFHVGRWEVEKLTGLSSEGRRAQDYVCGGLAPRIRKLEERAQRAKHAKSVFWSIFGKE 390
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 361 VKL 363
      |||
Db 391 IKL 393
      |||

RESULT 13
STAD_GOSHI STANDARD; PRT; 397 AA.
ID STAD_SIMCH Q01753;
AC Q01753;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Deltapine 16;
RA Liu Q., Singh S., Sharp P., Green A., Marshall D.R.;
RT "Nucleotide sequence of a cDNA from Gossypium hirsutum encoding a
RT stearoyl-acyl carrier protein desaturase."
RL (In) Plant Gene Register PGR36-018.
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC C15 DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
DR EMBL; X95988; CAA65232.1; .
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR Pfam; PF03405; FA_desaturase-2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 34 397 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 397 AA; 45233 MW; 5FAA22038B2C37A CRC64;
Query Match 84.1%; Score 1610.5; DB 1; Length 397;
Best Local Similarity 84.0%; Pred. No. 6.9e-117;

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Matches 305; Conservative 21; Mismatches 36; Indels 1; Gaps 1;
Qy 2 STLKSGSKEVNLLKPPMPPREVHVQVTHSMPPQKIEIFKSLDNWAENILVHLKPVEKC 61
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 35 STIFSGSKEVGNLKKPFTPPKEVPVQIHTSMPPKIEIFKSLGWAENILVHLKPVEKC 94
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 62 WQPDFLPPDASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEBALPTYQTMNLTDGV 121
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 95 WQPADELPPDPSDGFHEQVKELRAKEIPDDYFVVLVGDMMITEBALPTYQTMNLTDGT 154
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 122 RDETCASPTSAIWTAWTAENRHGDLNKLKLYLSGRVDMRQIEKTTQYLLIGSGMDPRT 181
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 155 RDETCASLTPWAIWTAWTAENRHGDLNKLKLYLSGRVDMRQIEKTTQYLLIGSGMDPRT 214
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 182 ENSPYLGFYTSFOERATFISGNTARQAKHEGDKLKAQICGTIAADEKRHETATYTKIVE 241
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 215 ENSPYRGFIYTSFOERATFISGNTGRLAKEYGDLNLAQICGSIASDEKRHETATYTKIVE 274
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 242 KLFEIDPDGTVLAFADMMRKKSIMPAHLMYDGRDDNLFDFHSVAORLGVYTAQDYADI 301
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 275 KLFEIDPDGTVLAFADMMRKKSIMPAHLMYDGRDDNLFDFHSVAORLGVYTAQDYADI 334
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 302 EFLVGRWKVKDLTGLSAGQKADYVCRLLPPRIRLRLEERAQRAKEAPTMPFSWIFDRQ 360
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 335 EHLVDRWKVKELAGLSAEGRAQDYVCLSLPSRIRLRLEERAQRAKEAGSTVPSPFWIFDRE 394
      |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
Qy 361 VKL 363
      |||
Db 395 VKL 397
      |||

RESULT 14
STAD_SIMCH STANDARD; PRT; 398 AA.
ID STAD_SIMCH Q01753;
AC Q01753;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Simmondsia chinensis (Jojoba).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Simmondsiaceae; Simmondsia.
OX NCBI_TaxID=3999;
RN [1]
RP SEQUENCE FROM N.A.
RA Sato A., Becker C.K., Knauf V.C.;
RT "Nucleotide sequence of a complementary DNA clone encoding stearyl-
RT acyl carrier protein desaturase from Simmondsia chinensis.";
RL Plant Physiol. 99:362-363(1992).
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC C15 DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES.
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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DR EMBL; M83199; AAA33932.1; -.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 34 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 35 398 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 398 AA; 45130 MW; F3E000BB044427D8 CRC64;

Query Match 83.9%; Score 1607; DB 1; Length 398;
Best Local Similarity 81.8%; Pred. No. 1.3e-116;
Matches 297; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

QY 1 ASTLKSSEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENLVHLKPVEK 60
DB 36 SSTIGITSKEIPNAKKPHMPREAHVQKTHSMPPQKIEIFKSLDGAEEENLVHLKPVEK 95
QY 61 CWPQDFLPDPSGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNTLDG 120
DB 96 CWPQDFLPDPSGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNTLDG 155
QY 121 VRDETASPTSWAITWTRAMTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
DB 156 VRDETASPTSWAITWTRAMTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 215
QY 181 TENSPYLGFIYTSFQERATFISHCNTARQAKEGDIKLAQICGTIAADEKRHETATYKIV 240
DB 216 SENPYLGFIYTSFQERATFISHCNTARQAKEGDIKLAQICGTIAADEKRHETATYKIV 275
QY 241 EKLFEPDPCGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 300
DB 276 EKLFEPDPCGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 335
QY 301 LEFLVGRWKVDKLTGSLAEGQKADYVCRPLPRIRLEERAQRAKEAPTMPFSWIFDRQ 360
DB 336 LEFLVGRWKVDKLTGSLAEGQKADYVCRPLPRIRLEERAQRAKEAPTMPFSWIFDRQ 395
QY 361 VKL 363
DB 396 LKV 398

RESULT 15
STAD_ORYSA STANDARD; PRT; 390 AA.
AC Q40731;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ACYL-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare; TISSUE=Seed;
RX MEDLINE=95334510; PubMed=7610181;
RA Akagi H., Baba T., Shimada H., Fujimura T.;
RT "Nucleotide sequence of a stearyl-acyl carrier protein desaturase
RT cDNA from developing seeds of rice.";
RL Plant Physiol. 108:845-846(1995).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
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CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; D38753; BAA07631.1; -.
CC HSSP; P22337; IAFR.
CC InterPro; IPR005067; FA_desat.
CC InterPro; IPR001225; FA_desaturase.
CC Pfam; PF03405; FA_desaturase_2; 1.
CC PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 31 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 32 390 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
SQ SEQUENCE 390 AA; 44482 MW; ED974E4C1E285597 CRC64;

Query Match 82.6%; Score 1583; DB 1; Length 390;
Best Local Similarity 81.0%; Pred. No. 8.9e-115;
Matches 294; Conservative 35; Mismatches 30; Indels 4; Gaps 1;

QY 1 ASTLKSSEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENLVHLKPVEK 60
DB 32 ASTI---NRVKTAKPYTPPREVHLQVKHSLPPQKREIFDSLQPWAKENLLNLLKPVEK 87
QY 61 CWPQDFLPDPSGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNTLDG 120
DB 88 SWQPDPLPDPSGDEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNTLDG 147
QY 121 VRDETASPTSWAITWTRAMTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
DB 148 VRDETASPTSWAITWTRAMTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPG 207
QY 181 TENSPYLGFIYTSFQERATFISHCNTARQAKEGDIKLAQICGTIAADEKRHETATYKIV 240
DB 208 TENPYLGFIYTSFQERATFISHCNTARQAKEGDIKLAQICGTIAADEKRHETATYKIV 267
QY 241 EKLFEPDPCGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 300
DB 268 EKLFEPDPCGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 327
QY 301 LEFLVGRWKVDKLTGSLAEGQKADYVCRPLPRIRLEERAQRAKEAPTMPFSWIFDRQ 360
DB 328 LEFLVGRWKVDKLTGSLAEGQKADYVCRPLPRIRLEERAQRAKEAPTMPFSWIFDRQ 387
QY 361 VKL 363
DB 388 VQL 390

Search completed: March 7, 2003, 03:09:10
Job time : 15 secs
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Db 274 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSAVAQRLGVYTKADYADI 333
Qy 301 LEFLVGRWKVKDTGLTGLSAGQKQADYVCRLLPPIRRLERAAQRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVKDTGLTGLSAGQKQADYVCRLLPPIRRLERAAQRAKEAPTMPSWIFDRQ 393
Qy 361 VKL 363
Db 394 VKL 396

RESULT 2
B39170
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - cucumber
C:Species: Cucumis sativus (cucumber)
C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Jun-2002
C:Accession: B39170
R:Shanklin, J.; Somerville, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
A:Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally und
A:Reference number: A39170; MUID:91172837; PMID:2006187
A:Accession: B39170
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-396 <SHA>
A:Cross-references: GB:M59857
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

Query Match 91.9%; Score 1760; DB 2; Length 396;
Best Local Similarity 90.4%; Pred. No. 3.9e-125;
Matches 328; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEFKSLDNNAEENILVHLKPVK 60
Db 34 ASTLRSTSEVELKKPFMPREVHVQVTHSMPPQKIEFKSLDNNAEENILVHLKPVK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLG 120
Db 94 CWPQDFLPDPAFEGFQVVELRAKELPDEVFVVLVGDMMITEALPTYQTMNLTLG 153
Qy 121 VRDETGAQSPSWAIWTRAWTAENRHGDLNKLKYLISLGRVDMRQIEKTIQYLIGSGMDPR 180
Db 154 VRDETGAQSPSWAIWTRAWTAENRHGDLNKLKYLISLGRVDMRQIEKTIQYLIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISGNTARQAKEHGDIKLAQICGTITADEKRRHETATYKIV 240
Db 214 TENSPLYGFIYTSFOERATFISGNTARQAKEHGDIKLAQICGTITADEKRRHETATYKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSAVAQRLGVYTKADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSAVAQRLGVYTKADYADI 333
Qy 301 LEFLVGRWKVKDTGLTGLSAGQKQADYVCRLLPPIRRLERAAQRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVKDTGLTGLSAGQKQADYVCRLLPPIRRLERAAQRAKEAPTMPSWIFDRQ 393
Qy 361 VKL 363
Db 394 VKL 396

RESULT 3
A39173
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - safflower
C:Species: Carthamus tinctorius (safflower)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C:Accession: A39173
R:Thompson, G.A.; Scherer, D.E.; Foxall-Van Aken, S.; Kenny, J.W.; Young, H.L.; Shintani
Proc. Natl. Acad. Sci. U.S.A. 88, 2578-2582, 1991
A:Title: Primary structures of the precursor and mature forms of stearoyl-acyl carrier p
A:Reference number: A39173; MUID:91172850; PMID:2006194
A:Accession: A39173
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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-396 <THO>
A:Cross-references: GB:M61109; NID:g167196; PIDN:AAA33021.1; PID:g167197
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

Query Match 91.4%; Score 1752; DB 1; Length 396;
Best Local Similarity 90.1%; Pred. No. 1.6e-124;
Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEFKSLDNNAEENILVHLKPVK 60
Db 34 ASTLGSTPKVDNAKKPFQPPREVHVQVTHSMPPQKIEFKSIEGMAEQNILVHLKPVK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLG 120
Db 94 CWPQDFLPDPASEGDFEQVKELRAKELPDDYFVVLVGDMMITEALPTYQTMNLTLG 153
Qy 121 VRDETGAQSPSWAIWTRAWTAENRHGDLNKLKYLISLGRVDMRQIEKTIQYLIGSGMDPR 180
Db 154 VRDETGAQSPSWAIWTRAWTAENRHGDLNKLKYLISLGRVDMRQIEKTIQYLIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISGNTARQAKEHGDIKLAQICGTITADEKRRHETATYKIV 240
Db 214 TENSPLYGFIYTSFOERATFISGNTARQAKEHGDIKLAQICGTITADEKRRHETATYKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSAVAQRLGVYTKADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMFAHLMYDGRDNDLFDHFSAVAQRLGVYTKADYADI 333
Qy 301 LEFLVGRWKVKDTGLTGLSAGQKQADYVCRLLPPIRRLERAAQRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVKDTGLTGLSAGQKQADYVCRLLPPIRRLERAAQRAKEAPTMPSWIFDRQ 393
Qy 361 VKL 363
Db 394 VKL 396

RESULT 4
T07806
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - soybean
N:Alternate names: stearoyl-acyl carrier protein desaturase
C:Species: Glycine max (soybean)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 03-Jun-2002
C:Accession: T07806
R:Chen, B.Y.; Jones, H.W.
Submitted to the EMBL Data Library, July 1994
A:Reference number: Z16145
A:Accession: T07806
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-411 <CHE>
A:Cross-references: EMBL:L34346; NID:g508602; PIDN:AAA92462.1; PID:g508603
C:Genetics:
A:Gene: SACPD
A:Genome: nuclear
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase
F:1-29/Domain: transit peptide (chloroplast) #status predicted <TNP>

Query Match 90.7%; Score 1738; DB 2; Length 411;
Best Local Similarity 89.4%; Pred. No. 1.9e-123;
Matches 322; Conservative 25; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEFKSLDNNAEENILVHLKPVK 60
Db 29 ASTLRSGSKEVENIKKFTTTPREVHVQVTHSMPPQKIEFQSLDWAENILAHKPVK 88
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKELPDDYFVVLVGDMMITEALPTYQTMNLTLG 120
Db 89 CWPQDFLPDPSSDGFEEQVKELRAKELPDDYFVVLVGDMMITEALPTYQTMNLTLG 148
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Qy 121 VRDETGA^{SP}TS^WAI^WTR^WTA^WEN^RRG^DLL^NK^YLY^LSG^RVD^MRQ^IE^KTK^TQ^IY^LLG^SMD^PR 180
 |||||
 Db 149 VRDETGA^{SP}TS^WAI^WTR^WTA^WEN^RRG^DLL^NK^YLY^LSG^RVD^MK^QE^KTK^TQ^IY^LLG^SMD^PR 208
 |||||
 Qy 181 TENS^PY^LGF^IY^TS^FQ^REA^TF^ISH^GNT^ARA^KEH^GDI^KLA^IQ^ICG^TTA^ADE^KRH^ETAY^TK^IV 240
 |||||
 Db 209 TENS^PY^LGF^IY^TS^FQ^REA^TF^ISH^GNT^ARA^KEH^GDI^KLA^IQ^ICG^MIA^SDE^KRH^ETAY^TK^IV 268
 |||||
 Qy 241 EK^LPE^TDP^CT^VLA^FAD^MMR^KK^ISM^{PA}HL^MW^DGR^DDN^LFD^HESA^VAO^RLG^VVT^AK^DY^ADI 300
 |||||
 Db 269 EK^LFES^DPD^CT^VWA^FAD^MMR^KK^ITAM^{PA}HL^MW^DGR^DDN^LFD^NTSS^VAQ^RIG^VVT^AK^DY^ADI 328
 |||||
 Qy 301 LE^FLV^GRM^KW^KDK^IT^LGS^{AE}GKA^QAD^VY^CRL^{PP}IR^{RL}EE^{RA}GKA^EAPT^MPF^SW^IFD^{RQ} 360
 |||||
 Db 329 LE^FLV^GRM^KW^KEQ^LT^LGS^{EG}RKA^QEY^{IC}GL^{PP}IR^{RL}EE^{RA}GKA^RV^{KE}ST^LAF^SW^IHD^{RE} 388
 |||||

RESULT 5
 E84869
 stearyl-ACP desaturase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2003
 C:Accession: E84869
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam,
 euss, D.; Nierman, W.C.: white, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis th
 A:Reference number: A84420; UID:20083487; PMID:10617197
 A:Accession: E84869
 A:Status: preliminary

A;Residues: 1-401 <STO>
A;Cross-references: GB:AE002093; NID:g2281099; PIDN:AAB64035.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g43710
A;Map position: 2
C;Superfamily: acyl-[acyl-carrier-protein] desaturase

	Query Match	90.48;	Score 1733;	DB 2;	Length 401;
	Best Local Similarity	89.48;	Pred. No. 4.3e-123;		
	Matches 32;	Conservative	Mismatches 16;	Indels	Gaps
Qy	4	LKSGSKVENLKKPFMPPREVHVQVTHSMPPQKIEIFKSLDNWAEBENTLVHLKPVKEQWQ	63		
Db	42	LSSGPKVESLKKPFTPREVHVQVLHSMPPQKIEIFKSMENWAEBENLLIHLKQVEKSWQ	101		
Qy	64	PDQLPDPASGDFQDEQRELRRAKEIPDDYFVVLVGMDMITEALPTYQTMLNTLDGYRD	123		
Db	102	PDQLPDPASGDFQDEQRELRRARELPDDYFVVLVGMDMITEALPTYQTMLNTLDGYRD	161		

Qy	124	ETGASPTSWAIWTRAWTAENRRHGDLLNKLYLUSGRVDMRQIEKTKYQYLIGSGMDPRTEN	183
Db	162	ETGASPTSWAIWTRAWTAENRRHGDLLNKLYLUSGRVDMRQIEKTKYQYLIGSGMDPRTEN	221
Qy	184	SPYLGFYLTFSQERATFISHGNTARQAKEHGDIKLAQICGTAADEKRHETATKILEKL	243
Db	222	NPYLGFYLTFSQERATFISHGNTARQAKEHGDIKLAQICGTAADEKRHETATKILEKL	281
Qy	244	FEIDPDGTVLAFADMMRRKKTSMPAHMLYDGRDNLDFHFSVAQRILGVVTKADYADILEF	303
Db	282	FEIDPDGTVMAFADMMRRKKTSMPAHMLYDGRDNLDFNFSVAQRILGVVTKADYADILEF	341
Qy	304	LVGRWKVKDTLGTLSAEGQAAQYVYVRLPPRIRLREARAQKAEAPTMFSPWFIEDRVKVL	363
Db	342	LVGRWKIODTLGTLSGEGNKAAQYLCGLAPRIKRLRLDERAARAKKGPILFISWIHDEVOL	401

RESULT 6
T14264
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower
N:Alternate names: stearyl-ACP desaturase

C:Species: *Helianthus annuus* (common sunflower)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T14264
R:Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J.
submitted to the EMBL Data Library, February 1997
A:Description: Sunflower stearyl-ACP desaturase.
A:Reference number: Z17946
A:Accession: T14264
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-396 <HON>
A:Cross-references: EMBL:U91339; NID:g2290399; PID:g2290400
A:Experimental source: Strain Mammoth
C:Function:
C:Description: Introduces a double bond at the delta(9) position of stearoyl-
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match	90.18;	Score	1727;	DB	2;	Length	396;
Best Local Similarity	88.7%;	Pred. No.	1.2e-122;				
Matches	322;	Conservative	23;	Mismatches	18;	Indels	0;
Gaps	0;						
Qy	1	ASTLKSGSKEVENLKPPMPPREVHVQVTHSMPPQKTEIFKSLDNWAENILVHLKPVEK	60				
Db	34	ASTIGSSTPKVESYKPTTPPREVHLQVTHSMPPQKTEIFKSIQWAEADNLVHLKPVEK	93				
Qy	61	CWQPDQLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDGMTTEALPTYQTMLNTLDG	120				
Db	94	CWQPDQLPDPASDGFDEQVRELRAKEIPDEYFVVLVGDGMTTEALPTYQTMLNTLDG	153				
Qy	121	VRDETGASPTSWATWTRAWTAENRHGDLNKNLYLSGRVDMRQIEKTIQYLGSGMDPR	180				
Db	154	VRDETGASPTSWATWTRAWTAENRHGDLNKHQYLYLSGRVDMRQIQTKTIQYLGSGMDPR	213				
Qy	181	TENSPYLGFIYTSFOERATFTISHGNTARQAQKEHGDIKLAQICGTIAADEKREHETAYTKIV	240				
Db	214	TENSPYLGFIYTSFOERATFTISHGNTARHAXYGDGLKLAQICGTIAADEKREHETAYTKIA	273				
Qy	241	EKLEIFDPDGTVLAFADMMRKISIMPAHLYMDGRDNLFDHFSVAQAQLGYVYTKADYADI	300				
Db	274	EKLEIFDPDGTVLAFADMMRKISIMPAHLYMDGRDNLFDHFSVAQAQLGYVYTKADYADI	333				
Qy	301	LEFLVGRWKVKDLTGLSAGEGKAQDYVCRLLPRTTTLREERAQGRAKAPTWPFSWIFDRQ	360				
Db	334	LEFLVGRWKVADLTGLSGEGRKAQDYVCGLPSRLRLEERAARAQKGPSPFWSWIFDRE	393				
Qy	361	VKL 363					
Db	394	VKL 396					

RESULT 7

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - spinach
 OHSFAD
 N:Alternate names: stearyl-[acyl-carrier-protein] desaturase
 N:Alternate names: stearyl-[acyl-carrier-protein] desaturase
 C:Species: Spinacia oleracea (spinach)
 C:Date: 31-Dec-1992 #sequence-revision 31-Dec-1992 #text-change 03-Jun-2001
 C:Accession: S22480; S18183
 R:Nishida, I.; Beppu, T.; Matsuo, T.; Murata, N.
 Plant Mol. Biol. 1990, 711-713, 1992
 A:Title: Nucleotide sequence of a cDNA clone encoding a precursor to stea
 A:Reference number: S22480; MUID: 92329733; PMID:1627785

A;Accession: S2Z480
A:Molecule type: mRNA

A;Residues: 1-399 <NIS>
A;Cross-references: EMBL:X62898; NID:g21229; PIDN:CAA4687.1; PID:g21230
C;Superfamily: acyl-[acyl-carrier-protein] desaturase
C;Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
F.1-395/Domain: transit peptide (chloroplast)#status predicted <NP>
F.36-395/Product: acyl-[acyl-carrier-protein] desaturase I#status predicted

Query Match 90.0%; Score 1724.5; DB 1; Length 399;
Best Local Similarity 87.9%; Pred. No. 1.9e-122;

Matches 320; Conservative 27; Mismatches 16; Indels 1; Gaps 1;

QY 1 ASTLKSGS-KEVENLKPPMPREVHVQVTHSMPPOKIEIFKSLDNWAEENILVHLKPYE 59
 DB 36 ASTLSSSPKEABSLKPPSPREVHVQVTHSMPPOKIEIFKSLGWAENILVHLKPYE 95
 QY 60 KCWQODFLPDPAASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTL 119
 DB 96 KCWQODFLPDPAASEDFRDQVKEIQERAKEIPDDLYVLVGDMMITEALPTQYTMNL 155
 QY 120 GVRDETGAFTSWAIWTRAWTAENRHGDLNKKYLSGRVDMRQIEKTIQYILGSGMDP 179
 DB 156 GAKDETGAFTSWAVWTRAWTAENRHGDLNKKYLSGRVDMRSTIEKTIQYILGSGMDP 215
 QY 180 RTENSYLGFYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKREHETATYKI 239
 DB 216 RTENSYLGVYTSFOERATFVSHGNSARLAKHEGDLKQAQICGIIASDEKREHETATYKI 275
 QY 240 VEKLFEDPDGTVLAFADMMRKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYAD 299
 DB 276 VEKLFEDPDATVLAFADMMRKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYAD 335
 QY 300 ILFELVGRWKVYDLTGLSABGQAQDYVCLPPRIIRLEERAQRAKEAPTMFSPWIFDR 359
 DB 336 ILFELVGRWEVEKLTGLSSEGQAQDYVCSLPPRIIRLEERARERAKQAPSMFSPWIFDR 395
 QY 360 QVKL 363
 DB 396 QVKL 399

RESULT 8
 T14268
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower
 N:Alternate names: stearoyl-ACP desaturase
 C:Species: Helianthus annuus (common sunflower)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
 C:Accession: T14268
 R:Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J.
 submitted to the EMBL Data Library, February 1997
 A:Description: Sunflower stearoyl-ACP desaturase.
 A:Reference number: Z17946
 A:Accession: T14268
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-396 <HON>
 A:Cross-references: EMBL:U91340; NID:g2290401; PID:g2290402
 A:Experimental source: strain Mammoth
 C:Function:
 A:Description: Introduces a double bond at the delta(9) position of stearoyl-ACP generated
 A:Pathway: fatty acid biosynthesis
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase
 C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match 88.8%; Score 1701; DB 2; Length 396;
 Best Local Similarity 88.4%; Pred. No. 1.1e-120;
 Matches 321; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPOKIEIFKSLDNWAEENILVHLKPYE 60
 DB 34 ASTIGSATTKVEKPPFTPPREVHVQVTHSMPPOKIEIFKSMGWAEDNLLVHLKPYE 93
 QY 61 CWQPDQLPDPAASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTL 120
 DB 94 CWQPDQLPDPAASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTL 153
 QY 121 VRDETGAFTSWAIWTRAWTAENRHGDLNKKYLSGRVDMRQIEKTIQYILGSGMDPR 180
 DB 154 VRDETGAFTSWAIWTRAWTAENRHGDLNKKYLSGRVDMRQIEKTIQYILGSGMDPR 213
 QY 181 TENSPLYLGFYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKREHETATYKI 240
 DB 214 TENSPLYLGFYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKREHETATYKI 273

QY 241 EKLFEIDPDGTVLAFADMMRKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADI 300
 DB 274 EKLFEIDPDGTVLAFADMMRKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADI 333
 QY 301 LEFLVGRWKVYDLTGLSABGQAQDYVCLPPRIIRLEERAQRAKEAPTMFSPWIFDRQ 360
 DB 334 LEFLVGRWKVADTGLSGEGQAQDYVCGPLAPRIIRLEERNSARAKESVNVVPFSPWIFDR 393
 QY 361 VKL 363
 DB 394 VKL 396

RESULT 9
 S23351
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - turnip
 C:Species: brassica rapa (turnip)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2002
 C:Accession: S23351
 R:Knutzon, D.S.; Thompson, G.A.; Radke, S.E.; Johnson, W.B.; Knauf, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2624-2628, 1992
 A:Title: Modification of Brassica seed oil by antisenescence expression of a stearoyl-acyl
 A:Reference number: S23351; MUID:92212881; PMID:1557366
 A:Accession: S23351
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-398 <KNU>
 A:Cross-references: EMBL:X60978; NID:g17928; PID:CAA43294.1; PID:g17929
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase
 C:Keywords: chloroplast; oxidoreductase

Query Match 88.6%; Score 1698; DB 2; Length 398;
 Best Local Similarity 88.2%; Pred. No. 1.9e-120;
 Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKPPMPREVHVQVTHSMPPOKIEIFKSLDNWAEENILVHLKPYEKCWQPDF 67
 DB 43 SKEVESLKKPFTPPKEVHVQVTHSMPPOKIEIFKSMEDWAEQNLTLQKDKVEKSWQPDF 102
 QY 68 LPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTL 127
 DB 103 LPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTQYTMNLTL 162
 QY 128 SPTSWAIWTRAWTAENRHGDLNKKYLSGRVDMRQIEKTIQYILGSGMDPRTPNSPYL 187
 DB 163 SPTSWAIWTRAWTAENRHGDLNKKYLSGRVDMRQIEKTIQYILGSGMDPRTPNNPYL 222
 QY 188 GFYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKREHETATYKI 247
 DB 223 GFYTSFOERATFISHGNTARQAKHEGDIKLAQICGTAADEKREHETATYKI 282
 QY 248 PDGTVLAFADMMRKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADILEFLVGR 307
 DB 283 PDGTVLAFADMMRKISMPAHLMYDGRDNLDFHFSAVAQRLGVYTKADYADILEFLVGR 342
 QY 308 WKYDKLTGLSABGQAQDYVCLPPRIIRLEERAQRAKEAPTMFSPWIFDRQVKL 363
 DB 343 WKIESLTGLSGEGKAQYELCGLTPRIIRLDERAQAARAKGPKVPFSPWIHREVQL 398

RESULT 10
 S24995
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - rape
 N:Alternate names: stearoyl-[acyl-carrier-protein] desaturase
 C:Species: Brassica napus (rape)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
 C:Accession: S24995
 R:Slocumbe, S.P.; Cummins, I.; Jarvis, R.P.; Murphy, D.J.
 Plant Mol. Biol. 20, 151-155, 1992
 A:Title: Nucleotide sequence and temporal regulation of a seed-specific Brassica napu
 A:Reference number: S24995; MUID:92385757; PMID:1515603

A:Accession: S24995
A:Molecule type: mRNA
A:Residues: 1-399 <SLO>
A:Cross-references: EMBL:X63364; NID:g17869; PIDN:CAA44964.1; PID:g17870
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; fatty acid biosynthesis; homodimer; oxidoreductase

Query Match 87.7%; Score 1680; DB 2: Length 399;
Best Local Similarity 87.1%; Pred. No. 4.2e-119; Mismatches 17; Indels 0; Gaps 0;
Matches 310; Conservative 29; Mismatches 17; Indels 0; Gaps 0;

Qy 8 SKEVENLKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKQWQPDF 67
Db 44 SKEVESLKPPTPPREVHLQVLSHMPQKIEIFKSMEDRAEQNLPLHLKDVESKQWQPDF 103

Qy 68 LPDPASDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDGVRDETGA 127
Db 104 LPDPASDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDGVRDETGA 163

Qy 128 SPTSWAIWTRAWTAENRHGDLNKLKYLKSGRVDNRQIEKTIQYILGSGMDPRTENSPLY 187
Db 164 SPTSWAVWTRAWTAENRHGDLNKLKYLKSGRVDNRQIEKTIQYILGSGMDPRTENNPYL 223

Qy 188 GFIVTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIVEKLEFID 247
Db 224 GFIVTSFOERATFVSHGNTARQAHEGDLKLAQICGTIAADEKRHETAYTKIVEKLEID 283

Qy 248 PDGTVLAFADMMRKISMPAHLMYDGRDNLFDHFSVAQRLGVYTAQDYADILEFLVGR 307
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Qy 308 KWVDKLTGLSAGOKAQDYVCRLLPRIRRLERAQRAKEAPTMPFSEIFDQVKL 363
Db 344 WRIESLGLSGEGNAQDYLCGLPRIRRLERAQRAKKGPKIPFSEIHDREVQL 399

RESULT 11
* S71264
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - Arabidopsis thaliana
N:Alternate names: Stearoyl-ACP desaturase
C:Species: Arabidopsis thaliana. (mouse-ear cress)
C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 03-Jun-2002
C:Accession: S71264
R:Piffanelli, P.; Murphy, D.J.
submitted to the EMBL Data Library, November 1995
A:Description: Cloning of a stearoyl-ACP desaturase from Arabidopsis thaliana.
A:Reference number: S71264
A:Accession: S71264
A:Molecule type: mRNA
A:Residues: 1-407 <PIF>
A:Cross-references: EMBL:X93461; NID:g1107506; PIDN:CAA63746.1; PID:g1107507
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match 86.7%; Score 1660.5; DB 2: Length 407;
Best Local Similarity 87.9%; Pred. No. 1.3e-117; Mismatches 21; Indels 5; Gaps 1;
Matches 311; Conservative 21; Mismatches 17; Indels 5; Gaps 1;

Qy 4 LKSSKEVENLKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKQWQ 63
Db 42 LSSGPKVESLKPPTPPREVHVQVLSHMPQKIEIFKSMENWAEENILHLKDVESKQW 101

Qy 64 QPDFLPDASDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDGVRD 123
Db 102 QPDFLPDASDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDGVRD 161

Qy 124 ETGASPTSWAIWTRAWTAENRHGDLNKLKYLKSGRVDNRQIEKTIQYILGSGMDPRTEN 183
Db 162 ETGASPTSWAIWTRAWTAENRHGDLNKLKYLKSGRVDNRQIEKTIQYILGSGMDPRTEN 221

Qy 184 SPYLGFIYTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIVEKL 243
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Qy 244 FEIDPDGTVLAFADMMRKISMPAHLMYDGRDNLFDHFSVAQRLGVYTAQDYADILEF 303
Db 282 FEIDPDGTVLAFADMMRKISMPAHLMYDGRDNLFDHFSVAQRLGVYTAQDYADILEF 341

Qy 304 LVGRWKVDKLTGLSAGOKAQDYVCRLLPRIRRLERAQRAK-----EAPTMP 352
Db 342 LVGRWKIQDLTGLSGEGNAQDYLCGLAPRIKRLDERAQAARAKLKGQKPILP 395

RESULT 12
* T14172
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower
N:Alternate names: Stearoyl-ACP desaturase
C:Species: Helianthus annuus (common sunflower)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T14172
R:Coughlan, S.J.; Hastings, C.E.; Winfrey, R.J.
submitted to the EMBL Data Library, September 1996
A:Description: Sunflower stearoyl-ACP desaturase.
A:Reference number: Z17901
A:Accession: T14172
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-396 <COU>
A:Cross-references: EMBL:U70374; NID:g1575696; PID:g1575697
A:Experimental source: strain SMF3
C:Function:
A:Description: introduces a double bond at the delta(9) position of stearoyl-ACP gene
A:Pathway: fatty acid biosynthesis
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match 86.4%; Score 1655; DB 2: Length 396;
Best Local Similarity 86.5%; Pred. No. 3.2e-117; Mismatches 19; Indels 0; Gaps 0;
Matches 314; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

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Db 34 ASTIGSATTKVESTKPKPTPPREVHQVLSHMPQKIEIFKSMEGWAEENILVHLKPVEK 93

Qy 61 CWQPDFLPDASDGFDOVRELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDG 120
Db 94 CWQAQDFLPDASDGFMEQVEELRAKEIPDDYFVVLVGDMMITEALPTQTMNTLDG 153

Qy 121 VRDETGASPTSWAIWTRAWTAENRHGDLNKLKYLKSGRVDNRQIEKTIQYILGSGMDPR 180
Db 154 VRDETGATLLGLVTRAWTAENRHGDLNKLKYLKSGRVDNRQIEKTIQYILGSGMDPR 213

Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAHEGDIKLAQICGTIAADEKRHETAYTKIV 273

Qy 241 EKLFEIDPDGTVLAFADMMRKISMPAHLMYDGRDNLFDHFSVAQRLGVYTAQDYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKISMPAHLMYDGRDNLFDHFSVAQRLGVYTAQDYADI 333

Qy 301 LEFLVGRWKVDKLTGLSAGOKAQDYVCRLLPRIRRLERAQRAKEAPTMPFSEIFDQ 360
Db 334 LEFLVGRWKVADI/TGLSGEGNAQDYVCGLAPRIIRRLERAQRAKESVNVFSEIFDRE 393

Qy 361 VKL 363
Db 394 VKL 396

RESULT 13
* S44202
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - Commerson's wild po
N:Alternate names: Stearoyl-ACP desaturase
C:Species: Solanum commersonii (Commerson's wild potato)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Jun-2002
C:Accession: S44202

Db 215 ENSPYRGEIYTSFQERATFISHGNTGRLAKEYGDINLAQICGSIASDEKRHETAYTKIVE 274
Qy 242 KLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAQRLGVYTKADYADIL 301
Db 275 KLFEIDPDGTVLAFADMMRKKIAMPAAEFYDGRDYNLFDFHSAVAQRLGVYTKADYVDIV 334
Qy 302 EFLVGRWKVKLTGLSABGQKAQDYVCRLPPIRRLRLEERAQRAK-EAPTMPFSWIFDRQ 360
Db 335 EHLVDRWKVKELAGLSABGRKAQDYLCSLPSRIRRLRLEERAQRAKQGSTPVSPFSWIFDRE 394
Qy 361 VKL 363
Db 395 VKL 397

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Job time : 23 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:10:02 ; Search time 16 Seconds
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Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSGSKEVENLKPKFMP.....RAKEAPTMPSWIFDROVKL 363

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Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1916	100.0	363	10	US-09-988-929A-1
2	1916	100.0	363	12	US-10-017-145-1
3	1637	85.4	396	10	US-09-837-751-2
4	291	15.2	54	9	US-09-730-763-12
5	291	15.2	54	9	US-09-730-763-16
6	286	14.9	54	9	US-09-730-763-13
7	283	14.8	54	9	US-09-730-763-15
8	276	14.4	54	9	US-09-730-763-18
9	273	14.2	52	9	US-09-730-763-27
10	271	14.1	52	9	US-09-730-763-31
11	270	14.1	54	9	US-09-730-763-17
12	270	14.1	54	9	US-09-730-763-14
13	267	13.9	338	9	US-09-730-763-4
14	267	13.9	338	9	US-09-730-763-37
15	262	13.7	52	9	US-09-730-763-28
16	260	13.6	52	9	US-09-730-763-29
17	255	13.3	54	9	US-09-730-763-19
18	254	13.3	52	9	US-09-730-763-33
19	247	12.9	52	9	US-09-730-763-30

20	232	12.1	52	9	US-09-730-763-32	Sequence 32, Appl
21	213	11.1	52	9	US-09-730-763-34	Sequence 34, Appl
22	102.5	5.3	54	9	US-09-730-763-20	Sequence 20, Appl
23	97.5	5.1	1049	10	US-09-815-242-10732	Sequence 10732, A
24	96	5.0	858	8	US-08-945-749-2	Sequence 2, Appl
25	94.5	4.9	447	10	US-09-815-242-13412	Sequence 13412, A
26	94.5	4.9	447	10	US-09-815-242-13590	Sequence 13590, A
27	90.5	4.7	1189	10	US-09-815-242-10552	Sequence 10552, A
28	87.5	4.6	393	9	US-09-895-913A-172	Sequence 172, App
29	87.5	4.6	393	10	US-09-881-752A-152	Sequence 152, App
30	87	4.5	368	9	US-09-738-626-4393	Sequence 4393, Ap
31	87	4.5	451	9	US-10-028-072-126	Sequence 126, App
32	87	4.5	451	9	US-10-121-049-126	Sequence 126, App
33	87	4.5	451	9	US-10-123-904-126	Sequence 126, App
34	87	4.5	451	9	US-10-140-470-126	Sequence 126, App
35	87	4.5	451	9	US-10-175-746-126	Sequence 126, App
36	87	4.5	451	9	US-10-176-918-126	Sequence 126, App
37	87	4.5	451	9	US-10-176-921-126	Sequence 126, App
38	87	4.5	451	9	US-10-137-865-126	Sequence 126, App
39	87	4.5	451	9	US-10-140-474-126	Sequence 126, App
40	87	4.5	451	9	US-10-142-431-126	Sequence 126, App
41	87	4.5	451	9	US-10-143-114-126	Sequence 126, App
42	87	4.5	451	9	US-10-140-002-126	Sequence 126, App
43	87	4.5	1169	10	US-09-815-242-13448	Sequence 13448, A
44	87	4.5	1169	10	US-09-815-242-13693	Sequence 13693, A
45	87	4.5	1460	10	US-09-815-242-13668	Sequence 13668, A

ALIGNMENTS

RESULT 1

US-09-988-929A-1

; Sequence 1, Application US/09988929A

; Patent No. US20020150982A1

; GENERAL INFORMATION:

; APPLICANT: Brookhaven Science Associates

; APPLICANT: Shanklin, John

; APPLICANT: Caboon, Edgar B

; TITLE OF INVENTION: Mutant Fatty Acid Desaturase

; FILE REFERENCE: BSA 02-01; CIP of 09/233,856, filed 01/19/99

; CURRENT APPLICATION NUMBER: US/09/988,929A

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 09/233,856

; PRIOR FILING DATE: 1999-01-19

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1

; LENGTH: 363

; TYPE: PRT

; ORGANISM: Ricinus communis

US-09-988-929A-1

Query Match 100.0%; Score 1916; DB 10; Length 363;
Best Local Similarity 100.0%; Pred. No. 7.8e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKPKFMPPREVHVQVTHSMPPKIEIFKSLDNWAEENILVHLKPVK 60

Db 1 ASTLKSGSKEVENLKPKFMPPREVHVQVTHSMPPKIEIFKSLDNWAEENILVHLKPVK 60

Qy 61 CWPQDFLPDPASDGFDEQVRELRRERAKETPDYFVVLVGDMTTEALPTYQTMNLTL 120

Db 61 CWPQDFLPDPASDGFDEQVRELRRERAKETPDYFVVLVGDMTTEALPTYQTMNLTL 120

Qy 121 VRDETASPTSWAIWTRAWTAENRHGDLNLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180

Db 121 VRDETASPTSWAIWTRAWTAENRHGDLNLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180

Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTAADEKRHETAYTKIV 240

Db 181 TENSPLYGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTAADEKRHETAYTKIV 240

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QY 241 EKLEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDDNLFDFHSAVAORLGVYTKADYADI 300
Db 241 EKLEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDDNLFDFHSAVAORLGVYTKADYADI 300
QY 301 LEFLVGRWKVDKLTGLSAGQKAQDYVCLPRLPRIRLLEERAQGRAKEAPTPMPSWIFDRQ 360
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Db 361 VKL 363

RESULT 2
US-10-017-145-1
; Sequence 1, Application US/10017145
; Patent No. US20020151019A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates
; APPLICANT: Shanklin, John
; TITLE OF INVENTION: Mutant Fatty Acid Desaturase and Methods for Directed Mutagenesis
; FILE REFERENCE: CIP of 09/328,550 filed June 9, 1999; which was a CIP of 09/233,856
; January 19, 1999
; CURRENT APPLICATION NUMBER: US/10/017,145
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 09/328,550
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Ricinus communis
; NAME/KEY: misc_feature
; OTHER INFORMATION: ricinus communis delta 9 18:0 Acyl ACP Desaturase
US-10-017-145-1

Query Match 100.0%; Score 1916; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 7 8e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 TNSPYLGFITYTSFOERATFISHGNTARQAEHGDIKLAQICGTTAADEKREHETAYTKIV 240
QY 241 EKLEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDDNLFDFHSAVAORLGVYTKADYADI 300
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QY 361 VKL 363
Db 361 VKL 363

RESULT 3
US-09-837-751-2
; Sequence 2, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qing
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Gossypium sp.
US-09-837-751-2

Query Match 85.4%; Score 1637; DB 10; Length 396;
Best Local Similarity 85.1%; Pred. No. 4 8e-143;
Matches 308; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

QY 2 STLKSGSKEVENLKKPPMPREHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 61
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QY 62 WQODELPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTTYOTMLNTLDG 121
Db 95 WQODELPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTTYOTMLNTLDG 154
QY 122 RDETASPTSWAIWTRAWTAENRHGDLNKLKYLVLGRVDMRQIEKTIQYLIIGSGMDPR 181
Db 155 RDETASPTSWAIWTRAWTAENRHGDLNKLKYLVLGRVDMRQIEKTIQYLIIGSGMDPR 214
QY 182 ENSPYLGFITYTSFOERATFISHGNTARQAEHGDIKLAQICGTTAADEKREHETAYTKIVE 241
Db 215 ENSPYLGFITYTSFOERATFISHGNTARQAEHGDIKLAQICGTTAADEKREHETAYTKIVE 274
QY 242 KLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDDNLFDFHSAVAORLGVYTKADYADI 301
Db 275 KLFEIDPDGTVLAFADMMRRKKSMPAHLMYDGRDDNLFDFHSAVAORLGVYTKADYADI 334
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QY 362 KL 363
Db 395 KL 396

RESULT 4
US-09-730-763-12
; Sequence 12, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahbow, Garrett &
; ADDRESSEE: Dunner, L.L.P
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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RESULT 8
US-09-730-763-18
; Sequence 18, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P
; ADDRESSEE: 1300 I Street, N.W.
; STREET: Washington
; CITY: D.C.
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

ZIP: 20005
 COMPUTER READABLE FORM:
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 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/730,763
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/917,299
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: MEYERS, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 03495.0156-00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-27

Query Match 14.2%; Score 273; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. NO. 1.6e-18;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRRHETAYT 237
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Db 1 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRRHETAYT 52

RESULT 10

US-09-730-763-31
; Sequence 31, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:

; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-31

Query Match 14.1%; Score 271; DB 9; Length 52;
Best Local Similarity 98.1%; Pred. NO. 2.5e-18;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 186 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRRHETAYT 237
|||||
Db 1 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRRHETAYT 52

RESULT 11

US-09-730-763-17
; Sequence 17, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:

; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-730-763-17

Query Match 14.1%; Score 271; DB 9; Length 54;
Best Local Similarity 90.7%; Pred. NO. 2.6e-18;
Matches 49; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 98 LVGDMITEALPTYOTMLNTLDGVRDETGAISPTSWAINTRAWTAENRHGDLN 151
|:|||||
Db 1 LIGDMITEALPTYOTMLNTLDGVRDETGAISPTSWAINTRAWTAENRHGDLN 54

RESULT 12

US-09-730-763-14
; Sequence 14, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:

; APPLICANT: JACKSON, Mary
; APPLICANT: GIQUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

Query Match 14.1%; Score 271; DB 9; Length 52;
Best Local Similarity 98.1%; Pred. NO. 2.5e-18;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 186 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRRHETAYT 237
|||||
Db 1 YLGFIYTSFQERATFISGNTARQAKHGDIKLAQICGCTIAADEKRRHETAYT 52

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-730-763-14

Query Match      14.1%; Score 270; DB 9; Length 54;
Best Local Similarity 92.6%; Pred. No. 3.2e-18;
Matches 50; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 98 LVGDMITEEALPTVQTMLTLDGVYRDETASPTSWAIWTRAWTAENRHGDLN 151
Db 1 LVGDMITEEALPTVQTMLTLDGVYRDETASPTSWAIWTRAWTAENRHGDLN 54

RESULT 13
US-09-730-763-4
; Sequence 4, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIOUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000

```

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; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-730-763-4

Query Match      13.9%; Score 267; DB 9; Length 338;
Best Local Similarity 25.6%; Pred. No. 9.3e-17;
Matches 84; Conservative 54; Mismatches 128; Indels 62; Gaps 11;

QY 19 MPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVKEKQPDQDFLPDPASDG--- 75
Db 1 MSAKLTDLQQLHLELP-----VVEKYLNRHLSMH-----KPNPHDYI--PWSGKNY 46

QY 76 -----FDEQVRELRAKEIFDDYFVVLVGDMMITEEALPTYQ---TMLNTLDGVYDET 125
Db 47 YALGGQDMDPDQSKLSVAQ-----VAMQNLVTEEDNLPVSHREIAMNMGD----- 94

QY 126 GASPTSWAIWTRAWTAENRHGDLNKLKLYLSGRVDMRQIEKTIQVILGSGMDPRTENSP 185
Db 95 -----AWQVWNRWTAENRHGDLALRDYLVVTRSDVPELEKLRLEVNRGSPGQNHQ 149

QY 186 YL-----GFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKHEHETATK 238
Db 150 HYFAESLTDSVLVSVFQELATRISHRNT---GKACNDPVADQLMAKISADENLHMIFRD 206

QY 239 IVKLEFIDPDGVILAFADAMRRKISKMPAHLMYDGRDNLDFHFSAVAQRUGVYTKDKYA 298
Db 207 VSEAADFVFN-----QAMKSLHLTLSHFQMPGFQVPEFRKAVVIAVGGVYDPRHL 259

QY 299 D-TLEFLVGRWKVDKLTGLTSAEGOKAOD 325
Db 260 DEVMPVLKKWCIFEREDFTGEGAKLKD 287

RESULT 14
US-09-730-763-37
; Sequence 37, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Mary
; APPLICANT: GIOUEL, Brigitte
; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,763
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/917,299
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0156-00
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-730-763-37

Query Match 13.9%; Score 267; DB 9; Length 338;
Best Local Similarity 25.6%; Pred. No. 9.3e-17;
Matches 84; Conservative 54; Mismatches 128; Indels 62; Gaps 11;
QY 19 MPPREHVGVTHSMPPQKIEIFKSLDNWAEENILVHLKPKVEKQWQDPDLPDPASDG--- 75
Db 1 MSAKLTDLQLLHELEP-----VVEKYLNRHLXSH-----KPWPHDYI--PWSGKNY 46
QY 76 -----FDEQVRELRLERAKEIPDDYFVVLVGDMMITEALPTYQ---TMLNTLDGVRDET 125
Db 47 YALGGQDNDPQDSKLSVQAQ-----VAMVQNLVTEDNLPVSHREIAMNMGMDG----- 94
QY 126 GASPTSWALWTRAWTAENRHRGDLNKLKYLILSGRVDMRQIEKTIQYLGSGMDPRTENSP 185
Db 95 -----AWGQVNRWTAENRHRGIALRDYLVTRSDVPVELEKRLLEVNRGFSQGNHOG 149
QY 186 YL-----GFIVTFOERATFISGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTK 238
Db 150 HYFAESLTDVSLVVSFOELATRISHNT---CKACNDPVADQLMAKISADENLHMFYRD 206
QY 239 IVEKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAQRLGLVYTAQDYA 298
Db 207 VSEAAFDLVN-----QAMKSLHLILSHFQMGFQVPEFRKKAIVIAVGGVYDPIHL 259
QY 299 D-ILFELVGRWKVKLTGLSAGQKQAD 325
Db 260 DEVMPVLKKKICIFEREDFTGEGAKLRD 287

RESULT 15

US-09-730-763-28
Sequence 28, Application US/09730763
Publication No. US20020192781A1
GENERAL INFORMATION:
APPLICANT: JACKSON, Mary
APPLICANT: GIOUEL, Brigitte
TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o Finnegan Henderson, Farrahaw, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,763
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/917,299
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0156-00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-730-763-28
Query Match 13.7%; Score 262; DB 9; Length 52;
Best Local Similarity 96.2%; Pred. No. 1.7e-17;
Matches 50; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 186 YLGFIVTSTOERATFISGNTARQAKEHGDIKLAQICGTIAADEKRHETAYT 237
Db 1 YLGFIVTSTOERATFISGNTARQAKEHGDIKLAQICGTIAADEKRHETAYT 52
Search completed: March 7, 2003, 03:14:49
Job time : 17 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:07:57 ; Search time 19 Seconds
(without alignments)
562.133 Million cell updates/sec

Title: US-10-017-145-1
Perfect score: 1916
Sequence: 1 ASTLKSQSGKEVENLKPFMP.....RAKEAPTPFSPWIFDQVKL 363

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1916	100.0	396	1	US-08-539-798-3
2	1916	100.0	396	1	US-08-329-560-3
3	1916	100.0	396	1	US-08-471-791-16
4	1916	100.0	396	4	US-08-926-522-4
5	1916	100.0	396	5	PCT-US91-01746-16
6	1753	91.5	391	1	US-07-995-657-6
7	1753	91.5	391	1	US-08-474-587-6
8	1752	91.4	396	1	US-08-471-791-13
9	1752	91.4	396	4	US-08-926-522-2
10	1752	91.4	396	5	PCT-US91-01746-13
11	1698	88.6	398	1	US-08-471-791-20
12	1698	88.6	398	4	US-08-926-522-6
13	1698	88.6	398	5	PCT-US91-01746-20
14	1316	68.7	385	1	US-08-539-798-4
15	1316	68.7	385	1	US-08-329-560-4
16	1261	65.8	387	1	US-08-539-798-2
17	1261	65.8	387	1	US-08-329-560-2
18	1218	63.6	368	2	US-08-869-137-2
19	291	15.2	54	3	US-08-917-299-12
20	291	15.2	54	3	US-08-917-299-16
21	291	15.2	54	4	US-09-422-662-12
22	291	15.2	54	4	US-09-422-662-16
23	286	14.9	54	3	US-08-917-299-13
24	286	14.9	54	4	US-09-422-662-13
25	283	14.8	54	3	US-08-917-299-15
26	283	14.8	54	4	US-09-422-662-15
27	276	14.4	54	3	US-08-917-299-18

28	276	14.4	54	4	US-09-422-662-18	Sequence 18, Appl
29	273	14.2	52	3	US-08-917-299-27	Sequence 27, Appl
30	273	14.2	52	4	US-09-422-662-27	Sequence 27, Appl
31	273	14.2	56	1	US-08-471-791-2	Sequence 2, Appl
32	273	14.2	56	5	PCT-US91-01746-2	Sequence 2, Appl
33	271	14.1	52	3	US-08-917-299-31	Sequence 31, Appl
34	271	14.1	52	4	US-09-422-662-31	Sequence 31, Appl
35	271	14.1	54	3	US-08-917-299-17	Sequence 17, Appl
36	271	14.1	54	4	US-09-422-662-17	Sequence 17, Appl
37	270	14.1	54	3	US-08-917-299-14	Sequence 14, Appl
38	270	14.1	54	4	US-09-422-662-14	Sequence 14, Appl
39	267	13.9	57	1	US-08-471-791-7	Sequence 7, Appl
40	267	13.9	57	5	PCT-US91-01746-7	Sequence 7, Appl
41	267	13.9	338	3	US-08-917-299-4	Sequence 4, Appl
42	267	13.9	338	3	US-08-917-299-37	Sequence 37, Appl
43	267	13.9	338	4	US-09-422-662-4	Sequence 4, Appl
44	267	13.9	338	4	US-09-422-662-37	Sequence 37, Appl
45	262	13.7	52	3	US-08-917-299-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-539-798-3
; Sequence 3, Application US/08539798
; Patent No. 5614400
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; TITLE OF INVENTION: Methods and Compositions Relating to
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: US
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,798
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,560
; FILING DATE: 26-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.
; REGISTRATION NUMBER: 36,063
; REFERENCE/DOCKET NUMBER: 0284US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

Query Match 100.0%; Score 1916; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 2, 2e-180;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTLKSQSGKEVENLKPFMPREVHVQVTHSMPPQKIEIFKSLDNNAEENILVHLKPVKE 60
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Db 34 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 93
QY 61 CWPQDPLPDPSDGFDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTLG 120
Db 94 CWPQDPLPDPSDGFDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTLG 153
QY 121 VRDETASPTSWAIWTRAWTAENRHDGDLNKLKYLKSLGRVDMRQIEKTIQYLGSGMDPR 180
Db 154 VRDETASPTSWAIWTRAWTAENRHDGDLNKLKYLKSLGRVDMRQIEKTIQYLGSGMDPR 213
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 240
Db 214 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 273
QY 241 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHFSVAQORGLVYTTAKDYADI 300
Db 274 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHFSVAQORGLVYTTAKDYADI 333
QY 301 LEFLVGRWKVDKLTGLSAEGQKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVDKLTGLSAEGQKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPSWIFDRQ 393
QY 361 VKL 363
Db 394 VKL 396

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RESULT 2
US-08-329-560-3
; Sequence 3, Application US/08329560
; Patent No. 5654402
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; APPLICANT: OHLROGEE, John B.
; TITLE OF INVENTION: Methods and Compositions Relating to
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: US
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,560
; FILING DATE: 26-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.
; REGISTRATION NUMBER: 36,063
; REFERENCE/DOCKET NUMBER: 0284US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 3:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-329-560-3
Query Match 100.0%; Score 1916; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 2,2e-180;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 60

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Db 34 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVEK 93
QY 61 CWPQDPLPDPSDGFDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTLG 120
Db 94 CWPQDPLPDPSDGFDEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTLG 153
QY 121 VRDETASPTSWAIWTRAWTAENRHDGDLNKLKYLKSLGRVDMRQIEKTIQYLGSGMDPR 180
Db 154 VRDETASPTSWAIWTRAWTAENRHDGDLNKLKYLKSLGRVDMRQIEKTIQYLGSGMDPR 213
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 240
Db 214 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRKHETAYTKIV 273
QY 241 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHFSVAQORGLVYTTAKDYADI 300
Db 274 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHFSVAQORGLVYTTAKDYADI 333
QY 301 LEFLVGRWKVDKLTGLSAEGQKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPSWIFDRQ 360
Db 334 LEFLVGRWKVDKLTGLSAEGQKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPSWIFDRQ 393
QY 361 VKL 363
Db 394 VKL 396

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RESULT 3
US-08-471-791-16
; Sequence 16, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knauf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoftword 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth

```

```
;
;
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 69-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-791-16

Query Match 100.0%; Score 1916; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.2e-180;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTLSGSGKEVENLKKPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
DB 34 ASTLSGSGKEVENLKKPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93
QY 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 120
DB 94 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 153
QY 121 VRDETGAPTSNAIWTAWTAENRHGDLNLYLSLGRVDMRQIEKTIQYILIGSGMDPR 180
DB 154 VRDETGAPTSNAIWTAWTAENRHGDLNLYLSLGRVDMRQIEKTIQYILIGSGMDPR 213
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICCTAADEKRRHETAYTKIV 240
DB 214 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTTAADEKRRHETAYTKIV 273
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYTAQYADI 300
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYTAQYADI 333
QY 361 VKL 363
DB 394 VKL 396

RESULT 4
US-08-926-522-4
; Sequence 4, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
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;
; APPLICATION NUMBER: US/08/926,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,173
; FILING DATE: 2-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE DES
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-926-522-4

Query Match 100.0%; Score 1916; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.2e-180;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTLSGSGKEVENLKKPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
DB 34 ASTLSGSGKEVENLKKPMPREHVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93
QY 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 120
DB 94 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEALPTYQTMNTLDG 153
QY 121 VRDETGAPTSNAIWTAWTAENRHGDLNLYLSLGRVDMRQIEKTIQYILIGSGMDPR 180
DB 154 VRDETGAPTSNAIWTAWTAENRHGDLNLYLSLGRVDMRQIEKTIQYILIGSGMDPR 213
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTTAADEKRRHETAYTKIV 240
DB 214 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTTAADEKRRHETAYTKIV 273
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYTAQYADI 300
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYTAQYADI 333
QY 361 VKL 363
DB 394 VKL 396

RESULT 5
PCT-US91-01746-16
; Sequence 16, Application PC/TUS9101746
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knauf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 19910314
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-01746-16

Query Match 100.0%; Score 1916; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.2e-180;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 34 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120
Db 94 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153
Qy 121 VRDETASPTSWA1WTRAWTAENRHHGDLNKLKYLKSLGRVDMROIEKTIQVLYIGSGMDPR 180
Db 154 VRDETASPTSWA1WTRAWTAENRHHGDLNKLKYLKSLGRVDMROIEKTIQVLYIGSGMDPR 213
Qy 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 240
Db 214 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGYVTAKDYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGYVTAKDYADI 333
Qy 301 LEFLVGRKKVDKLTGLSAGGAKADYVCRPLPRRRLREERAQGRAKEAPTWPFSWIFDRQ 360
Db 334 LEFLVGRKKVDKLTGLSAGGAKADYVCRPLPRRRLREERAQGRAKEAPTWPFSWIFDRQ 393
Qy 361 VKL 363
Db 394 VKL 396

RESULT 6
us-07-995-657-6
Sequence 6, Application US/07995657
Patent No. 5443974
GENERAL INFORMATION:
APPLICANT: Hitz, William D.

APPLICANT: Yadav, Narendra S.
APPLICANT: Perez, Grau, Luis
TITLE OF INVENTION: Nucleotide Sequence of
TITLE OF INVENTION: Soybean Stearoyl-ACP
TITLE OF INVENTION: Desaturase CDNA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours
ADDRESSEE: and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/995,657
FILING DATE: 19921211
FILING DATE: C) CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W.
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: BB_1022-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-995-657-6

Query Match 91.5%; Score 1753; DB 1; Length 391;
Best Local Similarity 89.8%; Pred. No. 2.4e-164;
Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 29 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 88
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120
Db 89 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 148
Qy 121 VRDETASPTSWA1WTRAWTAENRHHGDLNKLKYLKSLGRVDMROIEKTIQVLYIGSGMDPR 180
Db 149 VRDETASPTSWA1WTRAWTAENRHHGDLNKLKYLKSLGRVDMROIEKTIQVLYIGSGMDPR 208
Qy 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 240
Db 209 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 268
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGYVTAKDYADI 300
Db 269 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSVAQRLGYVTAKDYADI 328
Qy 301 LEFLVGRKKVDKLTGLSAGGAKADYVCRPLPRRRLREERAQGRAKEAPTWPFSWIFDRQ 360
Db 329 LEFLVGRKKVDKLTGLSAGGAKADYVCRPLPRRRLREERAQGRAKEAPTWPFSWIFDRQ 388
Qy 361 VKL 363
Db 361 VKL 363


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Db 389 VLL 391
RESULT 7
US-08-474-587-6
; Sequence 6, Application US/08474587
; Patent No. 5760206
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez-Grau, Luis
; TITLE OF INVENTION: Nucleotide Sequence of
; Patent No. 5760206
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; TITLE OF INVENTION: Desaturase cDNA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,587
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: SIEGELL, BARBARA C.
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB_1022-C
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-587-6
Query Match 91.5%; Score 1753; DB 1; Length 391;
Best Local Similarity 89.8%; Pred. No. 2.4e-164;
Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;
QY 1 ASTLSKSGSKEVENLKPPMPPEVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVKE 60
Db 29 ASTLSKSGSKEVENIKKPPFTPPREHVHVQVTHSMPPQKIEIFKSLDWDQONILHLKPVKE 88
QY 61 CWPQDFLPDPASDGFDEQVRELREAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLDG 120
Db 89 CWPQDFLPDPSSDGFEEQVKELREAKEIPDDYFVVLVGDMMITEALPTYQTMNLTLDG 148
QY 121 VRDETGAFTSWAIWTRAWTAENRHGDLNLYLXSGRVDVRQIEKTIQYILIGSGMDPR 180
Db 149 VRDETGAFTSWAIWTRAWTAENRHGDLNLYLXSGRVDVRQIEKTIQYILIGSGMDPR 208
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTTAADEKRHETAYTKIV 240
Db 209 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGMIASDEKRHETAYTKIV 268
QY 241 EKLFEIDPDGTVLAFADMMRRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYTKADYADI 300
Db 269 EKLFEVDPDGTVMAFADMMRRKKIAMPALHMYDGRDNLDFDNYSAVAQRIGVYTKADYADI 328
QY 301 LEFLVGRWKVDKLTGLSABGQKADYVCRCLPPRIRRLERAAQRAKEAETMPFSWIFDRQ 360
Db 329 LEFLVGRWKVEQLTGLSGEGRKAOYVCGLPPIRRLERAAQARGKESSTLAKFSWIHDRE 388
QY 361 VKL 363
Db 389 VLL 391
RESULT 8
US-08-471-791-13
; Sequence 13, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knauf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 69-5
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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MOLECULE TYPE: protein
US-08-471-791-13

Query Match 91.4%; Score 1752; DB 1; Length 396;

Best Local Similarity 90.1%; Pred. No. 3e-164; Indels 0; Gaps 0;
Matches 327; Conservative 18; Mismatches 18;

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QY 1 ASTLKSGKEVENLKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPEVK 60
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DB 34 ASTLGSSTPKVDNAKKFPQPPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPEVK 93
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CWPQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTDG 120
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 94 CWOAQDFLPDPASGDFEQVKELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTDG 153
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 VRDETASPTSWAIVTAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 154 VRDETASLTPMAVWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 213
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHGDGDKLAQICGTIAADEKRHHETATYKIV 240
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 214 TENSPLYGFIYTSFOERATFVSHGNTARHAKDHGDKVLAQICGTIASDEKRHHETATYKIV 273
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAORGLVYTTAKDYADI 300
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAORGLVYTTAKDYADI 333
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 LEFLVGRWKVDKLTGLSAGOKAODYVCRLLPPIRRIRLEERAQGRKAEPTMPFESWIFDRQ 360
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 334 LEFLVGRWKVADLTGLSGEGRKAQDYVCGLPPIRRIRLEERAQGRKAEPTMPFESWIFDRQ 393
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 VKL 363
    |||
DB 394 VKL 396
    |||

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RESULT 9

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US-08-926-522-2
; Sequence 2, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,173
; FILING DATE: 2-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE DES
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-926-522-2

```

Query Match 91.4%; Score 1752; DB 4; Length 396;

Best Local Similarity 90.1%; Pred. No. 3e-164; Indels 0; Gaps 0;
Matches 327; Conservative 18; Mismatches 18;

```

QY 1 ASTLKSGKEVENLKPFMPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPEVK 60
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 34 ASTLGSSTPKVDNAKKFPQPPREVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPEVK 93
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CWPQDFLPDPASGDFEQVRELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTDG 120
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 94 CWOAQDFLPDPASGDFEQVKELRAKEIPDDYFVVLVGDMMITEEALPTYQTMNLTDG 153
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 VRDETASPTSWAIVTAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 154 VRDETASLTPMAVWTRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 213
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHGDGDKLAQICGTIAADEKRHHETATYKIV 240
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 214 TENSPLYGFIYTSFOERATFVSHGNTARHAKDHGDKVLAQICGTIASDEKRHHETATYKIV 273
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAORGLVYTTAKDYADI 300
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSAVAORGLVYTTAKDYADI 333
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 LEFLVGRWKVDKLTGLSAGOKAODYVCRLLPPIRRIRLEERAQGRKAEPTMPFESWIFDRQ 360
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 334 LEFLVGRWKVADLTGLSGEGRKAQDYVCGLPPIRRIRLEERAQGRKAEPTMPFESWIFDRQ 393
    ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 VKL 363
    |||
DB 394 VKL 396
    |||

```

RESULT 10

```

PCT-US91-01746-13
; Sequence 13, Application PC/TUS9101746
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knauf, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 19910314
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 07/494,106

```


Sequence 6, Application US/08926522
Patent No. 6426447
GENERAL INFORMATION:
APPLICANT: Vic C. Knauf
TITLE OF INVENTION: PLANT SEED OILS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,173
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE DES
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-926-522-6

Query Match 88.6%; Score 1698; DB 4; Length 398;
Best Local Similarity 88.2%; Pred. No. 6.3e-159;
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKPFMPREVVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVKWCWQPDF 67
DB 43 SKEVESLKPFPTPPKEVHVQVLSHMPQKTEIFKSMEDWAEQNLLTQDKVKSQWQPDF 102
QY 68 LPDPASGDFEQVRELREARAKEIPDDYFVVLVGMITEEALPTYQTMNLTDGVRDETGA 127
DB 103 LPDPASGDFEQVRELREARARELPDDYFVVLVGMITEEALPTYQTMNLTDGVRDETGA 162
QY 128 SPTSWAIWTRAWTAENRHDLLNKLYLSGRVDMRQIKTIQYLGSGMDPRTEENPYL 187
DB 163 SPTSWAIWTRAWTAENRHDLLNKLYLSGRVDMRQIKTIQYLGSGMDPRTEENPYL 222
QY 188 GFYITSFQERATFISHGNTARAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLF 247
DB 223 GFYITSFQERATFISHGNTARAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLF 282
QY 248 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADILEFLVGR 307
DB 283 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADILEFLVGR 342
QY 308 WKVDKLTGLSAEQKAOQDYVCRLLPPRIRRLREERAQRAKEAPTFSPWIFDROVKL 363
DB 343 WKIESUTGLSGEGNAQEQYLCGLTPRIRRLDERAQAQRAKKGKVPFSPWIHREVLQ 398

RESULT 13
PCT-US91-01746-20
Sequence 20, Application PC/TUS9101746
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 19910314
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-01746-20

Query Match 88.6%; Score 1698; DB 5; Length 398;
Best Local Similarity 88.2%; Pred. No. 6.3e-159;
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKPFMPREVVHVQVTHSMPPQKTEIFKSLDNWAEENILVHLKPVKWCWQPDF 67
DB 43 SKEVESLKPFPTPPKEVHVQVLSHMPQKTEIFKSMEDWAEQNLLTQDKVKSQWQPDF 102
QY 68 LPDPASGDFEQVRELREARAKEIPDDYFVVLVGMITEEALPTYQTMNLTDGVRDETGA 127
DB 103 LPDPASGDFEQVRELREARARELPDDYFVVLVGMITEEALPTYQTMNLTDGVRDETGA 162
QY 128 SPTSWAIWTRAWTAENRHDLLNKLYLSGRVDMRQIKTIQYLGSGMDPRTEENPYL 187
DB 163 SPTSWAIWTRAWTAENRHDLLNKLYLSGRVDMRQIKTIQYLGSGMDPRTEENPYL 222
QY 188 GFYITSFQERATFISHGNTARAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLF 247
DB 223 GFYITSFQERATFISHGNTARAKEHGDILKLAQICGTIAADEKRHETAYTKIVEKLF 282
QY 248 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADILEFLVGR 307
DB 283 PDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADILEFLVGR 342

Db 257 YTKIVEKLAETIDPTTVIAFSDMMRKKIOMPAHAMYDGSDDMLFKHFTAVSQOIGYISAW 316
Qy 296 DYADILEFLYGRWKVDKLTGLSAEGOKAODYVCLPPIRIRLEERAQGRAKEAPTMP--F 353
Db 317 DYCDILDFLVDKWNVAKMTGLSGEGRKQOEYVCSLAAKIRRVEEKVOGKEKA-VLPVAF 375
Qy 354 SWIFDROV 361
Db 376 SWIFNROI 383

Search completed: March 7, 2003, 03:11:02
Job time : 20 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:03:42 ; Search time 39 seconds
(without alignments)
1240.256 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKSQSGKEVNLKKPFMP.....RAKEAPTPFSWIFDRQVKL 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1916	100.0	363	22	Mature castor enzy
2	1916	100.0	396	12	Ricinus communis d
3	1903	99.3	396	12	R. communis delta9
4	1753	91.5	391	13	Soybean seed stea
5	1753	91.5	391	19	Amino acid sequenc
6	1752	91.4	396	12	C. tinctorius delt
7	1752	91.4	396	13	Carthamus tinctori
8	1752	91.4	396	15	Sequence encoding
9	1752	91.4	396	19	Carthamus tinctori
10	1733	90.4	401	21	Arabidopsis thalia

11	1733	90.4	401	23	ABB92108	Herbicideally activ
12	1733	90.4	401	23	ABB07379	A. thaliana stearo
13	1721	89.8	391	16	AAR82024	Stearoyl-ACP-desat
14	1698	88.6	398	12	AAR14190	B. campestris delt
15	1698	88.6	398	18	AAW14798	Rapeseed stearyl-
16	1698	88.6	398	19	AAW44351	Brassica campestri
17	1694	88.4	401	18	AAW14797	Rapeseed stearyl-
18	1674	87.4	399	15	AAW47876	Delta-9-desaturase
19	1639.5	85.6	393	18	AAW09508	Zea mays delta-9 d
20	1639.5	85.6	393	21	AAW68987	Amino acid sequenc
21	1637	85.4	396	22	AAE13419	Cotton stearyl-AC
22	1636.5	85.4	363	21	AAW68988	Amino acid sequenc
23	1616.5	84.4	392	21	AAW32384	Corn delta-9 stea
24	1614	84.2	332	21	AAW22118	Arabidopsis thalia
25	1614	84.2	332	21	AAW29700	Arabidopsis thalia
26	1614	84.2	332	21	AAW45764	Arabidopsis thalia
27	1600.5	83.5	394	21	AAW16804	Arabidopsis thalia
28	1600.5	83.5	396	21	AAW16803	Arabidopsis thalia
29	1600.5	83.5	396	23	ABB92182	Herbicideally activ
30	1600.5	83.5	439	21	AAW16802	Arabidopsis thalia
31	1583	82.6	390	17	AAW96249	Delta 9-fatty acid
32	1577	82.3	392	21	AAW32385	Corn delta-9 stea
33	1557	81.3	321	21	AAW22119	Arabidopsis thalia
34	1557	81.3	321	21	AAW29701	Arabidopsis thalia
35	1557	81.3	321	21	AAW45765	Arabidopsis thalia
36	1529.5	79.8	391	21	AAW18099	Arabidopsis thalia
37	1529.5	79.8	393	21	AAW18098	Arabidopsis thalia
38	1529.5	79.8	395	21	AAW18097	Arabidopsis thalia
39	1526.5	79.7	394	23	ABB93501	Herbicideally activ
40	1411.5	73.7	414	22	AAW80920	Plastidial delta 9
41	1380	72.0	411	23	ABB92180	Herbicideally activ
42	1358	70.9	401	23	ABB93500	Herbicideally activ
43	1351	70.5	396	23	ABB92181	Herbicideally activ
44	1318	68.8	391	23	ABB91264	Herbicideally activ
45	1317	68.7	385	16	AAW65758	Coriander omega-12

ALIGNMENTS

RESULT 1
AAB48199
ID AAB48199 standard; Protein; 363 AA.
AC AAB48199;
DT 02-APR-2001 (first entry)
XX Mature castor enzyme.
DE Castor; delta9-18:0-acyl carrier protein desaturase; ACP; enzyme;
KW vegetable oil; fatty acid; nutrition; plant oil; mutant.
XX Ricinus communis.
OS Ricinus communis.
XX Key Location/Qualifiers
FH Misc-difference 114 /note= "can be substituted by Ala"
FT FT Misc-difference 117 /note= "can be substituted by Arg"
FT FT Misc-difference 118 /note= "can be substituted by Gly"
FT FT Misc-difference 179 /note= "can be substituted by Val"
FT FT Misc-difference 181 /note= "can be substituted by Val"
FT FT Misc-difference 188 /note= "can be substituted by Leu"
XX WO200075170-A1.
XX 14-DEC-2000.
XX

PF 08-JUN-2000; 2000WO-US15741.
XX
PR 09-JUN-1999; 99US-0328550.
XX
PA (BROO-) BROOKHAVEN SCI ASSOC LLC.
XX
PI Shanklin J;
XX
DR WPI; 2001-091202/10.
DR N-PSDB; AAC84531.
XX
PT New mutant castor Delta9-18:0-Acyl Carrier Protein desaturase, useful
PT in producing commercially valuable products, e.g. vegetable oils useful
PT in human nutrition or as industrial chemicals
XX
PS Examples: Fig 1: 53pp; English.
XX
CC The invention relates to a new mutant castor Delta9-18:0-acyl carrier
CC protein (ACP) desaturase that has one or more amino acid substitutions
CC selected from: (a) Ala for Met at residue 114; (b) Arg for Thr at residue
CC 117; (c) Gly for Leu at residue 118; (d) Val for Pro at residue 179; (e)
CC Val for Thr at residue 181; (f) Leu for Gly at residue 188; and (g) Phe
CC for Thr at residue 181. The mutant castor Delta9-18:0-ACP desaturase is
CC useful in producing commercially useful products, such as vegetable oils
CC rich in monounsaturated fatty acids. Such vegetable oils are important in
CC human nutrition and can be used as renewable sources of industrial
CC chemicals. A method for specifically altering a function of a protein
CC through directed mutagenesis is also provided. The method can be used
CC altering enzymatic functions, binding functions or structural functions
CC of the castor desaturase enzyme. The method is also useful for
CC manipulating the physical properties and commercial uses of conventional
CC plant oils. The present sequence represents the mature castor enzyme.
XX
SQ Sequence 363 AA;

Query Match 100.0%; Score 1916; DB 22; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.2e-171;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTQTMNTLDG 120
Db 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTQTMNTLDG 120
Qy 121 VRDETGASPTSWAIVTRAWTAENRHGDLNKKYLLSGRVDMMROIEKTIQYLGSGMDPR 180
Db 121 VRDETGASPTSWAIVTRAWTAENRHGDLNKKYLLSGRVDMMROIEKTIQYLGSGMDPR 180
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 240
Db 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 240
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADI 300
Db 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADI 300
Qy 301 LEFLVGRWKVDKLTGLSAGQKADYVCRLLPPIRRLLEAQAQRAKEAPTWPFSWIFDRQ 360
Db 301 LEFLVGRWKVDKLTGLSAGQKADYVCRLLPPIRRLLEAQAQRAKEAPTWPFSWIFDRQ 360
Qy 361 VKL 363
Db 361 VKL 363
RESULT 2
ID AAW44350 standard; Protein; 396 AA.
XX
AC AAW44350;

XX 28-MAY-1998 (first entry)
DT
XX Ricinus communis desaturase from clone pCGN3230.
DE
XX Ricinus communis; castor bean; delta-9 desaturase; oilseed;
KW fatty acid saturation.
KW
XX Ricinus communis.
OS
XX US5723595-A.
PN
XX 03-MAR-1998.
PD
XX 06-JUN-1995; 95US-0471791.
PF
XX 16-SEP-1991; 91US-0762762.
PR 16-MAR-1990; 90US-0494106.
PR 13-AUG-1990; 90US-0567373.
PR 14-NOV-1990; 90US-0615784.
PR 14-MAR-1991; 91WO-US01746.
PR 06-JUN-1995; 95US-0471791.
XX (CALJ) CALGENE INC.
PA
XX Knauf VC, Thompson GA;
PI
XX WPI; 1998-178544/16.
XX N-PSDB; AAV15252.
DR
XX DNA encoding plant delta-9 desaturase protein - having amino acid
PT sequence of Carthamus tinctorius desaturase, useful for, e.g.
PT producing oil-seeds with modified levels of fatty acid saturation
XX
PS Claim 7; Column 59-60; 87pp; English.
XX
CC The present sequence represents a Ricinus communis desaturase from
CC clone pCGN3230. The present invention describes a recombinant DNA
CC construct comprising a DNA sequence encoding a plant Delta-9 desaturase
CC protein. The present invention also provides a method of modifying fatty
CC acid composition in a host plant cell from a given fatty acid saturation
CC to a different fatty acid saturation, comprising growing a host plant
CC cell containing a recombinant DNA sequence which encodes a plant
CC desaturase under the control of regulatory elements functional in the
CC plant cell during lipid accumulation. Also, oilseeds having a modified
CC level of fatty acid saturation and oils produced from such oilseeds.
XX
SQ Sequence 396 AA;
Query Match 100.0%; Score 1916; DB 19; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.4e-171;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
Db 34 ASTLKSGSKEVENLKPPMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 93
Qy 61 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTQTMNTLDG 120
Db 94 CWPQDFLPDPASDGFDEQVRELRAKEIPDDYFVVLVGMITEEALPTQTMNTLDG 153
Qy 121 VRDETGASPTSWAIVTRAWTAENRHGDLNKKYLLSGRVDMMROIEKTIQYLGSGMDPR 180
Db 154 VRDETGASPTSWAIVTRAWTAENRHGDLNKKYLLSGRVDMMROIEKTIQYLGSGMDPR 213
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 240
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRRHETAYTKIV 273
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADI 300
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGVYTKADYADI 333


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Qy 301 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 360
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Db 334 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 393
Qy 361 VKL 363
|||
Db 394 VKL 396
|||

RESULT 3
ID AAR14189 standard; Protein; 396 AA.
XX AC AAR14189;
XX DT 11-DEC-1991 (first entry)
XX DE R. communis delta9 desaturase from pCGN3230.
XX KW Desaturase; fatty acid; saturation; chill tolerance; lipid;
XX KW herbicide.
XX OS Ricinus communis.
XX PN WO9113972-A.
XX PD 19-SEP-1991.
XX PF 14-MAR-1991; 91WO-U001746.
XX PR 14-NOV-1990; 90US-0615784.
XX PR 16-MAR-1990; 90US-0494106.
XX PR 13-AUG-1990; 90US-0567373.
XX PA (CALG-) CALGENE INC.
XX PI Thompson G, Knauf V;
XX WPI; 1991-295627/40.
XX DR N-PSDB; AAQ13964.
XX DNA encoding a plant desaturase - used for modifying the satd.
XX fatty acid compsn. of plant cells and plant seeds
XX PS Disclosure; Fig 3B; 128pp; English.
XX CC Modification of fatty acid in a plant host cell to a different
XX percentage of fatty acid satn. is possible by growing a host plant
XX cell having integrated into its genome a recombinant DNA sequence
XX encoding this protein, under the control of regulatory elements
XX functional in the plant cell during lipid accumulation, under
XX conditions which will promote the activity of the regulatory elements.
XX By increasing the amt. of desaturase available in plant cells, an
XX increased percentage of unsatd. fatty acids may be provided, using
XX anti-sense technology, the amt. of desaturase can be decreased,
XX resulting in a higher percentage of fatty acids.
XX Using the desaturase gene and derivs. in cells and plants,
XX desirable traits such as chill tolerance may be introduced and
XX environmentally safe herbicide prods. may be provided.
XX See also AAQ13963-69.
XX SQ Sequence 396 AA;

Query Match 99.3%; Score 1903; DB 12; Length 396;
Best Local Similarity 99.2%; Pred. No. 2.3e-170;
Matches 360; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKEVENKKPMPREHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVKE 60
|||||
Db 34 ASTLKSGSKEVENKKPMPREHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVKE 93
|||||

Qy 61 CWQPDQLPDPASGDFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 120
|||||
```

```
Db 94 CWQPDQLPDPASGDFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYOTMLNTLDG 153
Qy 121 VDETGASPTSWAIWTRAWTAENRHGDLNKNLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180
|||||
Db 154 VGDETGASPTSWAIWTRAWTAENRHGDLNKNLYLSGRVDMRQIEKTIQYLLIGSGMDPR 213
|||||
Qy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIV 240
|||||
Db 214 TENSPLYGFIYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRHETAYTKIV 273
|||||
Qy 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYTAQDYADI 300
|||||
Db 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRGLGVYTAQDYADI 333
|||||
Qy 301 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 360
|||||
Db 334 LEFLVGRWKVDKLTGLSAGGKAQDYVCRLLPPIRRLEERAQGRAKEAPTMPFSWIFDRQ 393
Qy 361 VKL 363
|||
Db 394 VKL 396
|||

RESULT 4
AAR20011
ID AAR20011 standard; Protein; 391 AA.
XX AC AAR20011;
XX DT 31-MAR-1992 (first entry)
XX DE Soybean seed stearyl-ACP desaturase.
XX KW soya bean; plant oil; stearic acid.
XX OS Glycine max strain Cultivar Wye.
XX FH Key Location/Qualifiers
XX FT Peptide 1..32
XX FT /label- transit
XX FT Protein 33..391
XX PN WO9118985-A.
XX PD 12-DEC-1991.
XX PF 16-MAY-1991; 91WO-US03288.
XX PR 25-MAY-1990; 90US-0529049.
XX PA (DUPO ) DU PONT DE NEMOURS CO.
XX PI Hitz WD, Yadav N;
XX WPI; 1992-007469/01.
XX DR N-PSDB; AAQ20187.
XX DNA encoding soybean stearyl-ACP desaturase enzyme and precursor
XX - and chimeric genes, for plant transformation and control of
XX levels of satd. and unsaturated fatty acids in edible oils
XX PS Disclosure; Page 54; 70pp; English.
XX CC Levels of saturated and unsaturated fatty acids can be controlled
XX in plants, e.g. oilseed rape, sunflower, soybean, peanut, etc.,
XX CC transformed with nucleic acid sequences coding for the expression
XX CC of this enzyme.
XX See also AAQ20188-Q20190 and AAR20012.
XX SQ Sequence 391 AA;

Query Match 91.5%; Score 1753; DB 13; Length 391;
Best Local Similarity 89.8%; Pred. No. 2.9e-156;
```

Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
DB 29 ASTLRSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 88
QY 61 CWOQDFLPDPASDGDQVRELRAKEIPDDYFVVVLVGDMMITEALPTYQTMNLTLG 120
DB 89 CWOQDFLPDPSSDGFEEQVKELRAKEIPDDYFVVVLVGDMMITEALPTYQTMNLTLG 148
QY 121 VRDETASPTSWAITRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
DB 149 VRDETASPTSWAITRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 208
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETATKIV 240
DB 209 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETATKIV 268
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 300
DB 269 EKLFEIDPDGTVMAFADMMRKKIAMPALHMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 328
QY 301 LEFLVGRWKVDKLTGLSAGOKAODYVCRPLPRIRRLLEERAQRAKEAPTMPFSWIFDRQ 360
DB 329 LEFLVGRWKVEQLTGLSGEGRKAQYVCGPLPRIRRLLEERAQRAKESSTLKFWSWIHDRE 388
QY 361 VKL 363
DB 389 VLL 391

RESULT 5
AAW37939
ID AAW37939 standard; Protein; 391 AA.
XX AAW37939;
DT 21-AUG-1998 (first entry)
XX Amino acid sequence of the soybean seed stearyl-ACP desaturase.
DE Soybean stearyl ACP-desaturase; chimeric gene; antisense;
KW transformation; saturated fatty acid; unsaturated fatty acid;
KW soybean oil; inhibition; polyunsaturate; monosaturate.
XX Glycine max.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..32
FT /note= "transit peptide"
FT Protein 33..391
FT /note= "mature protein"
XX
PN US5760206-A.
XX
XX
PD 02-JUN-1998.
XX
XX 07-JUN-1995; 95US-0474587.
XX
XX 07-JUN-1995; 95US-0474587.
PR 19-MAY-1991; 91WO-US03288.
PR 11-DEC-1992; 92US-0995657.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Hiltz WD, Perez-Grau L, Yadav NS;
XX
XX WPI; 1998-332247/29.
XX N-ESDB; AAV29236.
XX
XX Nucleic acids encoding soybean seed stearyl-ACP desaturase enzyme -
XX are useful for the anti-sense inhibition of the enzyme in
XX transformed plant cells

XX Disclosure; Column 43-46; 26pp; English.
PS This is the amino acid sequence of soybean stearyl ACP-desaturase,
XX used in the method of the invention, which involves the creation of
CC chimeric genes which are used in (antisense orientation) to transform
CC plant cells. The nucleic acids are useful for controlling the levels
CC of (unsaturated) fatty acids in soybean oil. In transformed cells
CC (seeds), the chimeric genes transcribe the antisense RNA to the
CC complementary mRNA for the enzyme. This results in inhibition of
CC expression of the endogenous enzyme and reduction in desaturation of
CC seed oil. This results in seed oil which is low in saturates and
CC polyunsaturates and high in monosaturates, giving an oil which is
XX healthier.
XX Sequence 391 AA;
SQ

Query Match 91.5%; Score 1753; DB 19; Length 391;
Best Local Similarity 89.8%; Pred. No. 2.9e-156;
Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

QY 1 ASTLKSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60
DB 29 ASTLRSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 88
QY 61 CWOQDFLPDPASDGDQVRELRAKEIPDDYFVVVLVGDMMITEALPTYQTMNLTLG 120
DB 89 CWOQDFLPDPSSDGFEEQVKELRAKEIPDDYFVVVLVGDMMITEALPTYQTMNLTLG 148
QY 121 VRDETASPTSWAITRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 180
DB 149 VRDETASPTSWAITRAWTAENRHGDLNKLKYLISGRVDMRQIEKTIQYLGSGMDPR 208
QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETATKIV 240
DB 209 TENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETATKIV 268
QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 300
DB 269 EKLFEIDPDGTVMAFADMMRKKIAMPALHMYDGRDNDLFDHFSAVAQRLGVYTAADYADI 328
QY 301 LEFLVGRWKVDKLTGLSAGOKAODYVCRPLPRIRRLLEERAQRAKEAPTMPFSWIFDRQ 360
DB 329 LEFLVGRWKVEQLTGLSGEGRKAQYVCGPLPRIRRLLEERAQRAKESSTLKFWSWIHDRE 388
QY 361 VKL 363
DB 389 VLL 391

RESULT 6
AAR14188
ID AAR14188 standard; Protein; 396 AA.
XX AAR14188;
XX
XX 11-DEC-1991 (first entry)
DT
DE C. tinctorius delta9 desaturase from pcgn274.
XX
XX Desaturase; fatty acid; saturation; chill tolerance; lipid;
KW herbicide.
KW
XX Carthamus tinctorius.
XX
XX Key Location/Qualifiers
FH Peptide 1..33
FT /label= transit_peptide
FT Protein 34..396
FT /label= mature_protein
XX
XX WO9113972-A.
PN
XX

PD 19-SEP-1991.
 XX
 PF 14-MAR-1991; 91WO-UO01746.
 XX
 PR 14-NOV-1990; 90US-0615784.
 PR 16-MAR-1990; 90US-0494106.
 PR 13-AUG-1990; 90US-0567373.
 XX
 PA (CALG-) CALGENE INC.
 XX
 PI Thompson G, Knauf V;
 XX
 DR WPI; 1991-295627/40.
 DR N-PSDB; AAQ13963.
 XX
 XX DNA encoding a plant desaturase - used for modifying the satd.
 PT fatty acid compsn. of plant cells and plant seeds
 XX
 PS Disclosure; Fig 2; 128pp; English.
 XX
 CC Modification of fatty acid in a plant host cell to a different
 CC percentage of fatty acid satn. is possible by growing a host plant
 CC cell having integrated into its genome a recombinant DNA sequence
 CC encoding this protein, under the control of regulatory elements
 CC functional in the plant cell during lipid accumulation, under
 CC conditions which will promote the activity of the regulatory elements.
 CC By increasing the amt. of desaturase available in plant cells, an
 CC increased percentage of unsatd. fatty acids may be provided, using
 CC anti-sense technology, the amt. of desaturase can be decreased,
 CC resulting in a higher percentage of fatty acids.
 CC using the desaturase gene and derivs. in cells and plants,
 CC desirable traits such as chill tolerance may be introduced and
 CC environmentally safe herbicide prods. may be provided.
 CC See also AAQ13963-69.
 XX
 SQ Sequence 396 AA;
 Query Match 91.4%; Score 1752; DB 12; Length 396;
 Best Local Similarity 90.1%; Pred. No. 3.7e-156;
 Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;
 QY 1 ASTLKSKEVENLKKPFMPREHVQVTHSMPPQKIEIFKSLDNNAENILVHLKPVEK 60
 DB 34 ASTLGSSTPKVDNAKPKFPQPREHVQVTHSMPPQKIEIFKSLDNNAENILVHLKPVEK 93
 QY 61 CWOQDFLPPDASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 120
 DB 94 CWOAQDFLPPDASEGDFEQVKELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 153
 QY 121 VRDETGAFTSWAIWTRAWTAENRHDLLNKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180
 DB 154 VRDETGASLTWAVWTRAWTAENRHDLLHTYLYLSGRVDMRQIQKTIQYLLIGSGMDPR 213
 QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADKRHETATYTKIV 240
 DB 214 TENSPLYGFIYTSFQERATFVSHGNTARHAKDHGVKLAQICGTIASDEKRHETATYTKIV 273
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRLGVYTKADYADI 300
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRLGVYTKADYADI 333
 QY 361 VKL 363
 DB 394 VKL 396
 RESULT 7
 AAR22048
 ID AAR22048 standard; Protein; 396 AA.

XX AAR22048;
 AC
 XX 07-JUL-1992 (first entry)
 DT
 XX Carthamus tinctorius desaturase.
 DE
 XX Safflower; fatty acid synthesis; seed; acyl carrier protein;
 KW lipids.
 KW
 XX Carthamus tinctorius.
 OS
 XX WO9203564-A.
 PN
 XX 05-MAR-1992.
 PD
 PF 15-AUG-1991; 91WO-UO05801.
 XX
 PR 26-JUN-1991; 91US-0721761.
 PR 15-AUG-1990; 90US-0568493.
 XX
 PA (CALG-) CALGENE INC.
 XX
 PI Knauf VC, Thompson GA;
 XX
 DR WPI; 1992-096907/12.
 DR N-PSDB; AAQ22616.
 XX
 XX New plant beta-keto:acyl synthase protein - obt'd. from Ricinus
 PT communis, useful e.g. for modifying fatty acid compsn.
 PT
 PS Disclosure; Fig 8; 157pp; English.
 XX
 CC The protein sequence was deduced from the desaturase gene isolated
 CC from Carthamus tinctorius as the clone pCGN2754. The clone can be
 CC used to construct acyl carrier protein expression cassettes in a
 CC binary vector for plant transformation. This allows integration
 CC of nucleic acids encoding a desaturase sequence and a synthase
 CC sequence into the genome of a host cell. A plant desaturase
 CC includes any enzyme capable of catalysing the insertion of a first
 CC double bond into a fatty acid-ACP moiety especially between C9-C10.
 CC See also AAR22046-53.
 XX
 SQ Sequence 396 AA;
 Query Match 91.4%; Score 1752; DB 13; Length 396;
 Best Local Similarity 90.1%; Pred. No. 3.7e-156;
 Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;
 QY 1 ASTLKSKEVENLKKPFMPREHVQVTHSMPPQKIEIFKSLDNNAENILVHLKPVEK 60
 DB 34 ASTLGSSTPKVDNAKPKFPQPREHVQVTHSMPPQKIEIFKSLDNNAENILVHLKPVEK 93
 QY 61 CWOQDFLPPDASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 120
 DB 94 CWOAQDFLPPDASEGDFEQVKELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDG 153
 QY 121 VRDETGAFTSWAIWTRAWTAENRHDLLNKLYLSGRVDMRQIEKTIQYLLIGSGMDPR 180
 DB 154 VRDETGASLTWAVWTRAWTAENRHDLLHTYLYLSGRVDMRQIQKTIQYLLIGSGMDPR 213
 QY 181 TENSPLYGFIYTSFQERATFISHGNTARQAKHEGDIKLAQICGTIAADKRHETATYTKIV 240
 DB 214 TENSPLYGFIYTSFQERATFVSHGNTARHAKDHGVKLAQICGTIASDEKRHETATYTKIV 273
 QY 241 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRLGVYTKADYADI 300
 DB 274 EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSVAQRLGVYTKADYADI 333
 QY 301 LEFLVGRWKVKLTGLSAGCQKADYVCLPPIRRLEERAQRAKEAPTMPFSWIFDRQ 360
 DB 334 LEFLVGRWKVADLTGLSGEGRKADYVCGLPPIRRLEERAQRAKEGVPVPSWIFDRQ 393

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Qy 361 VKL 363
    |||
Db 394 VKL 396

RESULT 8
AAR54033
ID AAR54033 standard; Protein; 396 AA.
XX
AC AAR54033;
XX
DT 01-DEC-1994 (first entry)
XX
DE Sequence encoding desaturase enzyme.
XX
KW Synthase; plants; oil; seed; fatty acids; gene expression;
KW biosynthesis; ss.
XX
OS C. tinctorius.
XX
PN W09410189-A.
XX
PD 11-MAY-1994.
XX
PF 02-NOV-1993; 93WO-US10526.
XX
PR 02-NOV-1992; 92US-0971182.
XX
PA (CALJ ) CALGENE INC.
XX
PI Knauf VC, Thompson GA;
XX
DR WPI: 1994-167378/20.
DR N-PSDB; AAQ64003.
XX
XX
DNA constructs encoding beta-keto:acyl-ACP synthase - useful to
modify the oil content of seeds, e.g. for dietary purposes
XX
PS Disclosure; Figure 10; 85pp; English.
XX
CC Higher plants appear to share a common metabolic pathway for the
CC synthesis of fatty acids. Genes encoding synthase proteins may be
CC used in nucleic acid constructs to modulate the amount of synthase
CC activity in a host cell. Nucleic acid constructs may also be
CC designed to decrease the expression of a synthase protein, i.e.,
CC constructs containing anti-sense synthase sequences. The constructs
CC allow the generation of plants bearing seeds which have enhanced oil
CC yields and/or altered compositions of oils. The production of
CC common plant unsaturated fatty acids is catalysed by a desaturase.
CC Oleic, linoleic and alpha-linoleic acids found in storage
CC triglycerides are produced from the desaturation of stearoyl-ACP to
CC form oleoyl-ACP.
XX
SQ Sequence 396 AA;

Query Match 91.4%; Score 1752; DB 15; Length 396;
Best Local Similarity 90.1%; Pred. No. 3.7e-156;
Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ASTLSGSKEVENLKKPFMPREVHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVEK 60
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34 ASTLSGSTPKVDNAKKFPQPPREVHVQVTHSMPPQKIEFKSGEWAQNILVHLKPVEK 93
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 CWOQDFLPDASGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMLNTLDG 120
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 94 CWOQDFLPDASEGDFEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMLNTLDG 153
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 VRDETGAFTSWAIWTRAWTAENRHGDLNKKYLSGRVDMRQTEKTIQYILGSGMDPR 180
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154 VRDEGTASLTWAVWTRAWTAENRHGDLNKKYLSGRVDMRQTEKTIQYILGSGMDPR 213
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 TENSPLYLGFYTSFQERATFVSHGNTARHAKDGHGVKLAQICGTIASDEKRHETATYTKIV 240
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 214 TENSPLYLGFYTSFQERATFVSHGNTARHAKDGHGVKLAQICGTIASDEKRHETATYTKIV 273
Qy 241 EKLFEPDPTGTVLAFADMRKKISMPAHLMYDGRDDNLFDFHFSAVAQRLGVYTAQDYADI 300
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 EKLFEPDPTGTVLAFADMRKKISMPAHLMYDGRDDNLFDFHFSAVAQRLGVYTAQDYADI 333
Qy 301 LEFLVGRWKVKDLTGLTSAEGOKAQDYVCRLLPPIRRLEERAQGRAKCAPTMPFSWIFDRQ 360
    ||| | : : | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 334 LEFLVGRWKVADLTGLSGEGKKAQDYVCGLLPPIRRLEERAQGRAKEGVPVPSWIFDRQ 393
Qy 361 VKL 363
    |||
Db 394 VKL 396

RESULT 9
AAR44349
ID AAR44349 standard; Protein; 396 AA.
XX
AC AAR44349;
XX
DT 28-MAY-1998 (first entry)
XX
DE Carthamus tinctorius desaturase from clone PCGN2754.
XX
KW Carthamus tinctorius; safflower; delta-9 desaturase; oilseed;
KW fatty acid saturation.
XX
OS Carthamus tinctorius.
XX
PI Key Location/Qualifiers
FT Peptide 1..33
FT /label= signal
FT Protein 34..396
FT /label= desaturase
XX
XX US5723595-A.
XX
XX 03-MAR-1998.
XX
XX 06-JUN-1995; 95US-0471791.
XX
XX 16-SEP-1991; 91US-0762762.
XX 16-MAR-1990; 90US-0494106.
XX 13-AUG-1990; 90US-0567373.
XX 14-NOV-1990; 90US-0615784.
XX 14-MAR-1991; 91WO-US01746.
XX 06-JUN-1995; 95US-0471791.
XX
XX (CALJ ) CALGENE INC.
XX
XX Knauf VC, Thompson GA;
XX
XX WPI: 1998-178544/16.
XX N-PSDB; AAV15250.
XX
XX DNA encoding plant delta-9 desaturase protein - having amino acid
XX sequence of Carthamus tinctorius desaturase, useful for, e.g.
XX producing oil-seeds with modified levels of fatty acid saturation
XX
XX Claim 5; Column 53-56; 87pp; English.
XX
CC The present sequence represents a Carthamus tinctorius desaturase from
CC clone PCGN2754. The present invention describes a recombinant DNA
CC construct comprising a DNA sequence encoding a plant Delta-9 desaturase
CC protein. The present invention also provides a method of modifying fatty
CC acid composition in a host plant cell from a given fatty acid saturation
CC to a different fatty acid saturation, comprising growing a host plant
CC cell containing a recombinant DNA sequence which encodes a plant
CC desaturase under the control of regulatory elements functional in the
CC plant cell during lipid accumulation. Also, oilseeds having a modified
CC level of fatty acid saturation and oils produced from such oilseeds.
XX

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SQL	Sequence	396 AA;	PR	30-APR-1999;	99US-0132407.
	Query Match	91.4%; Score 1752; DB 19; Length 396;	PR	04-MAY-1999;	99US-0132484.
	Best Local Similarity	90.1%; Pred. No. 3.7e-156;	PR	05-MAY-1999;	99US-0132485.
	Matches 327; Conservative	18; Mismatches 18; Indels 0; Gaps 0;	PR	06-MAY-1999;	99US-0132486.
			PR	06-MAY-1999;	99US-0132487.
QY	1	ASTLKSGSKEYENLKPFMPREYHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK 60	PR	07-MAY-1999;	99US-0132863.
		: : : : : :	PR	11-MAY-1999;	99US-0134256.
DB	34	ASTLGSSTPKVDNAKPFQPPREYHVQVTHSMPPQKIEIFKSGWAEQNILVHLKPVEK 93	PR	14-MAY-1999;	99US-0134218.
			PR	14-MAY-1999;	99US-0134219.
			PR	14-MAY-1999;	99US-0134221.
QY	61	CWQQDFLPDPASGDFEQVRELBERAKEIPDDYFVVLVGMITEALPTQTMLNTLDG 120	PR	14-MAY-1999;	99US-0134370.
			PR	18-MAY-1999;	99US-0134768.
DB	94	CWQQDFLPDPASGDFEQVRELBERAKEIPDDYFVVLVGMITEALPTQTMLNTLDG 153	PR	19-MAY-1999;	99US-0134941.
			PR	20-MAY-1999;	99US-0135124.
QY	121	VRDETGAAPTSAWITRAWTAENRHGDLNKNLYLVLSGRVDMRQLEKTIQYLLIGSGMDPR 180	PR	21-MAY-1999;	99US-0135353.
			PR	24-MAY-1999;	99US-0135629.
DB	154	VRDETGAAPTSAWITRAWTAENRHGDLNKNLYLVLSGRVDMRQLEKTIQYLLIGSGMDPR 213	PR	25-MAY-1999;	99US-0136021.
			PR	27-MAY-1999;	99US-0136392.
QY	181	TENSPYLGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTIAADEKRHETAYTKIV 240	PR	28-MAY-1999;	99US-0136782.
			PR	01-JUN-1999;	99US-0137222.
DB	214	TENSPYLGFIYTSFOERATFISHGNTARQAEKHGDIKLAQICGTIAADEKRHETAYTKIV 273	PR	03-JUN-1999;	99US-0137528.
			PR	04-JUN-1999;	99US-0137502.
QY	241	EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGYVYTAQDYADI 300	PR	07-JUN-1999;	99US-0137724.
			PR	08-JUN-1999;	99US-0138094.
DB	274	EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLDFHFSAVAQRLGYVYTAQDYADI 333	PR	10-JUN-1999;	99US-0138540.
			PR	10-JUN-1999;	99US-0138847.
QY	301	LEFLVGRWKVKDLTGLSAEGOKAODYVCRLPPRIIRLLEERAQGRAKEAPTMPFSWIFDRQ 360	PR	14-JUN-1999;	99US-0139119.
			PR	16-JUN-1999;	99US-0139452.
DB	334	LEFLVGRWKVKDLTGLSEGRKAODYVCGLLPPIIRLLEERAQGRAKEGPPVFFSWIFDRQ 393	PR	16-JUN-1999;	99US-0139453.
			PR	17-JUN-1999;	99US-0139492.
QY	361	VKL 363	PR	18-JUN-1999;	99US-0139454.
			PR	18-JUN-1999;	99US-0139455.
DB	394	VKL 396	PR	18-JUN-1999;	99US-0139456.
			PR	18-JUN-1999;	99US-0139457.
			PR	18-JUN-1999;	99US-0139458.
RESULT 10			PR	18-JUN-1999;	99US-0139459.
AAG29699			PR	18-JUN-1999;	99US-0139460.
ID	AAG29699 standard; Protein; 401 AA.		PR	18-JUN-1999;	99US-0139461.
XX			PR	18-JUN-1999;	99US-0139462.
AC	AAG29699;		PR	18-JUN-1999;	99US-0139463.
XX			PR	18-JUN-1999;	99US-0139750.
DT	17-OCT-2000 (first entry)		PR	18-JUN-1999;	99US-0139763.
DE			PR	21-JUN-1999;	99US-0139817.
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 35381.		PR	22-JUN-1999;	99US-0139899.
KW	Protein identification; signal transduction pathway; metabolic pathway;		PR	23-JUN-1999;	99US-0140353.
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		PR	23-JUN-1999;	99US-0140354.
KW	termination sequence.		PR	24-JUN-1999;	99US-0140695.
XX			PR	28-JUN-1999;	99US-0140823.
OS	Arabidopsis thaliana.		PR	29-JUN-1999;	99US-0140991.
PN	EPI033405-A2.		PR	01-JUL-1999;	99US-0141287.
XX			PR	01-JUL-1999;	99US-0141842.
PD	06-SEP-2000.		PR	01-JUL-1999;	99US-0142154.
XX			PR	02-JUL-1999;	99US-0142055.
XX	25-FEB-2000; 2000EP-0301439.		PR	06-JUL-1999;	99US-0142390.
XX			PR	08-JUL-1999;	99US-0142803.
XX			PR	09-JUL-1999;	99US-0142920.
XX			PR	12-JUL-1999;	99US-0142977.
PR	25-FEB-1999;	99US-0121825.	PR	13-JUL-1999;	99US-0143542.
PR	05-MAR-1999;	99US-0123180.	PR	14-JUL-1999;	99US-0143624.
PR	09-MAR-1999;	99US-0123548.	PR	15-JUL-1999;	99US-0144005.
PR	23-MAR-1999;	99US-0125788.	PR	16-JUL-1999;	99US-0144085.
PR	25-MAR-1999;	99US-0126264.	PR	16-JUL-1999;	99US-0144086.
PR	29-MAR-1999;	99US-0126785.	PR	19-JUL-1999;	99US-0144325.
PR	01-APR-1999;	99US-0127462.	PR	19-JUL-1999;	99US-0144331.
PR	06-APR-1999;	99US-0128234.	PR	19-JUL-1999;	99US-0144332.
PR	08-APR-1999;	99US-0128714.	PR	19-JUL-1999;	99US-0144333.
PR	16-APR-1999;	99US-0129845.	PR	19-JUL-1999;	99US-0144334.
PR	19-APR-1999;	99US-0130077.	PR	19-JUL-1999;	99US-0144335.
PR	21-APR-1999;	99US-0130449.	PR	20-JUL-1999;	99US-0144352.
PR	23-APR-1999;	99US-0130510.	PR	20-JUL-1999;	99US-0144632.
PR	23-APR-1999;	99US-0130891.	PR	20-JUL-1999;	99US-0144884.
PR	28-APR-1999;	99US-0131449.	PR	21-JUL-1999;	99US-0144814.
PR	30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0145086.


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Oy 244 FEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGYVTAKDYADILEF 303
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 282 FEIDPDGTVMAFADMMRKKISMPAHLMYDGRDNLFDNFSSVAQRLGYVTAKDYADILEF 341
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 304 LVGRKWKDKLTGLSAEGOKAODYVCRLLPRRLRLEERAQRAKEAPTMPPFSWIFDQVKL 363
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 342 LVGRWKIODLTGLSGEGNAODYLCGLAPRIKRLDERAQAARAKKPKIPFSWIHDREVQL 401

RESULT 13
AAR82024
ID AAR82024 standard; Protein: 391 AA.
XX
AC AAR82024;
XX
DT 10-APR-1996 (first entry)
XX
DE Stearoyl-ACP-desaturase precursor.
XX
KW Stearoyl-ACP-desaturase; soybean; seed oil; vegetable oil;
KW fatty acid; stearic acid; transgenic plant; crop improvement.
XX
OS Glycine max cv. Wye.
XX
FH Key
FT Peptide 1..32 Location/Qualifiers
FT Protein 33..391 /label= Transit_peptide
FT /label= Mat_protein
XX
PN US5443974-A.
XX
PD 22-AUG-1995.
XX
PF 25-MAY-1990; 90US-0529049.
XX
PR 11-DEC-1992; 92US-0995657.
PR 25-MAY-1990; 90US-0529049.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Hitz WD, Perez-Grau L, Yadav NS;
XX
DR WPI; 1995-302121/39.
DR N-PSDB; AAT00395.
XX
PT New isolated soybean stearoyl-ACP desaturase gene - use for the
PT prodn. of seed oil contg. altered levels of satd. and unsatd. fatty
PT acids
XX
PS Disclosure; Column 41-44; 25pp; English.
XX
CC The stearoyl-ACP-desaturase precursor (AAR82024) is the product of
CC a cDNA clone (AAT00395) derived from soybean developing leaves. It
CC catalyses the conversion of stearoyl-ACP to oleoyl-ACP.
CC Expression of the mature enzyme in transgenic plants such as soybean,
CC rapeseed, sunflower, cocoa, peanut, sunflower and corn, allows the
CC fatty acid composition, esp. the stearic acid content, of the seed oil
CC to be controlled.
XX
SQ Sequence 391 AA;
      Query Match 89.8%; Score 1721; DB 16; Length 391;
      Best Local Similarity 88.78; Pred. No. 3e-153;
      Matches 322; Conservative 25; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ASTLKSGSKEVENLKPFMPREHVQVTHSMPPQKIEFKSLDNWAEENILVHLKPVEK 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 29 ASTLRSGSKEVENIKKPTPPREHVQVTHSMPPQKIEFKSLDQADQNLTLHLKPVEK 88
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy *61 CWQPDQLPNPSSDGFESQVKELRERAKEITLYFVVVLVGDMMITEEALPTYQTMNLTDG 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Db 89 CWQPDQLPNPSSDGFESQVKELRERAKEITLYFVVVLVGDMMITEEALPTYQTMNLTDG 148
Oy 121 VRDEGTASPTSWAIWTRAWTAEENRHGDLNKLKYLKSGRVDMMQTEKTIQYLVIGSGMDPR 180
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 149 VRDEGTASLTSWAIWTRAWTAEENRHGDLNKLKYLKSGRVDMMQTEKTIQYLVIGSGMDPR 208
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 181 TENSPLYGFIYTSFOERATFISHGNTARQAKEHGDIKLQAICGTIAADEKRHETAYTKIV 240
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 209 TENSPLYGFIYTSFOERATFISHGNTARLAKAHEGDIKLAQICGMIASDEKRHETAYTKIV 268
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 241 EKLEIDPDGTVLAFADMMRKKISMPAHLMYDGRDNLFDHFSAVAQRLGYVTAKDYADI 300
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 269 EKLEFVDPDGTVMAPADMMRKKIAMPAHLMYDGRDNLFDNYSAVAQRLGYVTAKDYADI 328
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 301 LEFLVGRWKVDKLTGLSAEGOKAODYVCRLLPRRLRLEERAQRAKEAPTMPPFSWIFORQ 360
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 329 LEFLVGRWKVEQLTGLSGEGRKAQEVYVGLPPRRLRLEERAQRAKESSTLKFWSIHDR 388
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 361 VKL 363
      |||
Db 389 VLL 391

RESULT 14
AAR14190
ID AAR14190 standard; Protein: 398 AA.
XX
AC AAR14190;
XX
DT 11-DEC-1991 (first entry)
XX
DE B. campestris delta9 desaturase from PCGN3235.
XX
KW Desaturase; fatty acid; saturation; chill tolerance; lipid;
KW herbicide.
XX
OS Brassica campestris.
XX
PN WO9113972-A.
XX
PD 19-SEP-1991.
XX
PF 14-MAR-1991; 91WO-UO01746.
XX
PR 14-NOV-1990; 90US-0615784.
PR 16-MAR-1990; 90US-0494106.
PR 13-AUG-1990; 90US-0567373.
XX
PA (CALG-) CALGENE INC.
XX
PI Thompson G, Knauf V;
XX
DR WPI; 1991-295627/40.
DR N-PSDB; AAQ13965.
XX
PT DNA encoding a plant desaturase - used for modifying the satd.
PT fatty acid compsn. of plant cells and plant seeds
XX
PS Disclosure; Fig 4C; 128pp; English.
XX
CC Modification of fatty acid in a plant host cell to a different
CC percentage of fatty acid satn. is possible by growing a host plant
CC cell having integrated into its genome a recombinant DNA sequence
CC encoding this protein, under the control of regulatory elements
CC functional in the plant cell during lipid accumulation, under
CC conditions which will promote the activity of the regulatory elements.
CC By increasing the amt. of desaturase available in plant cells, an
CC increased percentage of unsatd. fatty acids may be provided, using
CC anti-sense technology, the amt. of desaturase can be decreased,
CC resulting in a higher percentage of fatty acids.
CC Using the desaturase gene and derivs. in cells and plants,
CC desirable traits such as chill tolerance may be introduced and
CC environmentally safe herbicide prods. may be provided.

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CC See also AAQ13963-69.

XX SQ Sequence 398 AA;

Query Match 88.6%; Score 1698; DB 12; Length 398;
Best Local Similarity 88.2%; Pred. No. 4.5e-151;
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKKPPMPREHVQVTHSMPPKIEIFKSLDNWAEENILVHLKPVCKWQPODF 67
DB 43 SKEVESLKKPFTPPKEVHVQVLSHMPPOKIEIFKSNEDWAGNLLTQLKDVESKWPQDF 102
QY 68 LPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDGVRDETGA 127
DB 103 LPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDGVRDETGA 162
QY 128 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTENSPYL 187
DB 163 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTENSPYL 222
QY 188 GFITYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRRHETAYTKIVEKLFELD 247
DB 223 GFITYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRRHETAYTKIVEKLFELD 282
QY 248 PDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSVAQAQRLGVVYTAADYADILEFLVGR 307
DB 283 PDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSVAQAQRLGVVYTAADYADILEFLVGR 342
QY 308 WKVDKLTGLSAGQKAQDYVCRLLPPIRLLEERAQRAKEAPTMPFSWIFDROVKL 363
DB 343 WKIESLTGLSGEGNKAQEYLCGLTPRIIRLDERAQAQRAKKGPKVPFWSWIHDREVQL 398

RESULT 15

AAW14798
ID AAW14798 standard; Protein; 398 AA.

XX AC AAW14798;

XX DT 03-JUL-1997 (first entry)

XX DE Rapeseed stearyl-ACP desaturase BND9.

XX KW Stearyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;
XX KW antisenase; triglyceride; stearic acid; transgenic plant; oilseed;
XX KW vegetable oil; mangosteen; Garcinia mangifera.

XX OS Brassica napus cv. 212/86.

XX PN WO9712047-A1.

XX PD 03-APR-1997.

XX PF 30-SEP-1996; 96WO-US16078.

XX PR 29-SEP-1995; 95US-0537083.

XX PA (CALJ) CALGENE INC.

XX PI Knauf VC, Kridl J, Lassner MW;

XX DR WPI; 1997-212906/19.

XX DR N-PSDB; AAT63438.

XX PT Increasing levels of stearate in plant seed triglyceride(s)
PT using a DNA sequence encoding acyl-ACP thioesterase protein having
PT substantial activity on C18:0 acyl-ACP substrates

XX PS Example 5; Fig7A-7C; 55pp; English.

XX CC Oilseed rape stearyl-ACP desaturases BND11 (AAW14797) and BND9
CC (AAW14798) each catalyse the desaturation of stearyl-ACP (C18:0) to
CC oleoyl-ACP (C18:1). Their amino acid sequences were deduced from

CC cDNA clones (AAT63437-38) isolated from a Brassica napus cv. 212/86
CC mid-mutation seed cDNA library. An antisense gene was constructed
CC to generate antisense RNA homologous to both BND9 and BND11. In
CC transgenic Brassica plants expressing the stearyl-ACP desaturase
CC antisense construct and mangosteen Class I acyl-ACP thioesterase
CC GarmFAL1 (see also AAW14795), levels of C18:0 in the seed oil may
CC exceed 50% of total fatty acids.

XX SQ Sequence 398 AA;

Query Match 88.6%; Score 1698; DB 18; Length 398;
Best Local Similarity 88.2%; Pred. No. 4.5e-151;
Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 8 SKEVENLKKPPMPREHVQVTHSMPPKIEIFKSLDNWAEENILVHLKPVCKWQPODF 67
DB 43 SKEVESLKKPFTPPKEVHVQVLSHMPPOKIEIFKSNEDWAGNLLTQLKDVESKWPQDF 102
QY 68 LPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDGVRDETGA 127
DB 103 LPDPASDGFDEQVRELRAKEIPDDYFVVLVGDMMITEALPTYQTMNTLDGVRDETGA 162
QY 128 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTENSPYL 187
DB 163 SPTSWAIWTRAWTAENRHGDLNKKLYLSGRVDMRQIEKTIQYILGSGMDPRTENSPYL 222
QY 188 GFITYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRRHETAYTKIVEKLFELD 247
DB 223 GFITYTSFOERATFISHGNTARQAKHEGDIKLAQICGTIAADEKRRHETAYTKIVEKLFELD 282
QY 248 PDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSVAQAQRLGVVYTAADYADILEFLVGR 307
DB 283 PDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDFHSVAQAQRLGVVYTAADYADILEFLVGR 342
QY 308 WKVDKLTGLSAGQKAQDYVCRLLPPIRLLEERAQRAKEAPTMPFSWIFDROVKL 363
DB 343 WKIESLTGLSGEGNKAQEYLCGLTPRIIRLDERAQAQRAKKGPKVPFWSWIHDREVQL 398

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